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OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 13:36:38 ; Search time 696 Seconds
(without alignments)
10827.343 Million cell updates/sec

Title: US-10-018-392A-3
Perfect score: 1273
Sequence: 1 ggctctcactaactaatca.....atctcttatcttgaatctt 1273

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1273	100.0	1273	4	Aaf54017
2	1273	100.0	1707	6	Aai171008
3	1273	100.0	2775	3	Aaa54034
4	1273	100.0	2804	8	Abv77053
5	1273	100.0	38059	4	Aaf54018
6	1273	100.0	38059	6	Abn95627
7	1273	100.0	38059	10	Add71098
8	1272	99.9	1272	4	Aaf54080
9	1271.4	99.9	1273	4	Aaf54074
10	1271.4	99.9	1273	4	Aaf54073
11	1269.8	99.7	1273	4	Aaf54075
12	1269.8	99.7	2792	2	Aax28626
13	1268.2	99.6	2781	1	Aan40142
14	1268.2	99.6	2802	2	Aat02460
15	1266.6	99.5	1273	4	Aaf54076
16	1261.8	99.1	2781	1	Aan40177
17	1261	99.1	1272	4	Aaf54079
18	1261	99.1	1275	4	Aaf54077
19	1260	99.0	1276	4	Aaf54078
20	1258.6	98.9	2728	13	Adq38340

21	1258.6	98.9	2771	13	Adq38338
22	1258.6	98.9	2777	13	Adq38339
23	1258.6	98.9	2831	13	Adq38341
24	1257.4	98.8	2758	13	Acn43105
25	1257.4	98.8	2766	13	Acn43104
26	1174.6	92.3	2807	1	Aan60543
27	1174.6	92.3	2807	12	Adh42198
28	883.4	69.4	1971	4	Abas5251
29	883.4	69.4	1971	4	Abas28575
30	200.6	15.8	201	13	Adq40547
31	200.6	15.8	201	13	Adq40266
32	200.6	15.8	201	13	Adq40829
33	200.6	15.8	201	13	Adq41116
34	186	14.6	1438	6	Abq82328
35	186	14.6	1438	12	Adh42196
36	186	14.6	1638	1	Aan50351
37	186	14.6	1639	1	Aan50049
38	186	14.6	1639	1	Aan50362
39	157	12.3	1612	12	Adh42200
40	154	12.1	154	4	Aaf54087
41	153	12.0	153	4	Aaf54119
42	153	12.0	153	4	Aaf54088
43	152.6	12.0	422	8	Abx47596
44	152	11.9	152	4	Aaf54120
45	152	11.9	152	4	Aaf54089

ALIGNMENTS

RESULT 1
Aaf54017
ID AAF54017 standard; DNA; 1273 BP.
XX
AC AAF54017;
XX
DT 30-MAR-2001 (first entry)
XX
DE hFIX gene 3' UTR age-related regulatory region AE3', SEQ ID NO:3.
XX
KW Age-related gene regulation; gene expression; human factor IX; hFIX;
KW AE3'; 3' UTR; 3' untranslated region; A3'; element;
KW age-regulatable expression construct; antisense therapy; gene therapy;
KW thrombosis; cardiovascular disease; diabetes; Alzheimer's disease;
KW Parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia; ds.
XX
OS Homo sapiens.
XX
PN WO200075279-A2.
XX
PD 14-DEC-2000.
XX
PF 06-JUN-2000; 2000WO-US015728.
XX
PR 09-JUN-1999; 99US-00328925.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Kurachi K, Kurachi S;
XX
PS WPI; 2001-061708/07.
XX
PT New regulatory elements that control age-related gene expression, useful
PT in gene therapy and for reducing factor IX expression.
XX
PS Claim 1; Fig 3A; 225pp; English.
XX
CC The invention relates to nucleic acid sequences which regulate gene
CC expression in an age-related manner and/or in a liver-specific manner.
CC The invention identifies regions of the human factor IX (hFIX) gene, and
CC a region of the human protein C (hPC) gene, which are age-related
CC regulatory sequences. The hFIX age-related regulatory sequences are
CC designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'

XX PD 27-DEC-2001.
 XX PF 19-JUN-2001; 2001WO-US019634.
 XX PR 20-JUN-2000; 2000US-0212902P.
 XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PI Miao CH, Kay MA;
 XX DR WPI; 2002-114582/15.
 XX PT Nucleic acid construct for expressing nucleic acid molecules, proteins in
 PT mammalian liver cells, has operably linked hepatic locus control element,
 PT hepatic promoter, coding sequence, polyadenylation signal and intron.
 XX PS Example 1; Page 57-59; 64pp; English.
 XX CC The present sequence is that of the 3' untranslated region (3' UTR) of
 CC the human Factor IX gene. The 3' UTR, which includes a polyadenylation
 CC signal, it was incorporated into expression cassettes of the invention
 CC that were designed for liver-specific expression of Factor IX. The
 CC cassettes also include an hepatic locus control element, an hepatic
 CC promoter located 3' to the hepatic locus control element, a Factor IX
 CC coding sequence, and an intron (see A171003-16). Also provided are
 CC vectors that include an expression cassette of the invention. These may
 CC be episomal or integrating vectors, including viral vectors, and are used in
 CC a claimed method of ameliorating disease. A therapeutic amount blood
 CC clotting Factor IX is produced in mammalian liver cells for at least 100
 CC days, and preferably at least 500 days. In examples of the invention,
 CC human Factor IX was expressed in mouse liver cells following injection of
 CC retrovirus-based plasmids that carried the expression cassettes into the
 CC tail vein or portal vein, and by direct injection of plasmid DNA into the
 CC liver
 XX SQ Sequence 1707 BP; 500 A; 362 C; 305 G; 540 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1273; DB 6; Length 1707;
 Best Local Similarity 100.0%; Pred. No. 7.2e-279;
 Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGCTCTCACTAATCACTTTCCCATCTTTTGGTAGATTTGAATATATACATTTCTAT 60
 DB 51 GGCCTCTCACTAATCACTTTCCCATCTTTTGGTAGATTTGAATATATACATTTCTAT 110
 QY 61 GATCATGTCTTTTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAATTTGATTA 120
 DB 111 GATCATGTCTTTTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAATTTGATTA 170
 QY 121 GAAATGGAAACCACTAGAGGAATATATGTTGTTAGGAAATTTACAGTCATTTCTTAAGGGCC 180
 DB 171 GAAATGGAAACCACTAGAGGAATATATGTTGTTAGGAAATTTACAGTCATTTCTTAAGGGCC 230
 QY 181 CAGCCCTTGACAAAATTTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 240
 DB 231 CAGCCCTTGACAAAATTTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 290
 QY 241 TCCACTATGCACTAATCACTCAATTTTCCCTCTTACGAGCATTTCCATCTCCCGAT 300
 DB 291 TCCACTATGCACTAATCACTCAATTTTCCCTCTTACGAGCATTTCCATCTCCCGAT 350
 QY 301 CTCTCTTGTCTTCTCCAAACCAACATCAATGTTTATTTAGTTCTGTATACAGTACAGATC 360
 DB 351 CTCTCTTGTCTTCTCCAAACCAACATCAATGTTTATTTAGTTCTGTATACAGTACAGATC 410
 QY 361 TTTGGTCTACTCTATCACAAGGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420
 DB 411 TTTGGTCTACTCTATCACAAGGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
 QY 421 TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTCTCTACCTTATTCCTCAATCTT 480

DB 471 TGAGAGGCTAAAACTCATCAAAAACACTACTCTTTTCTCTTACCTATTCCTCAATCTT 530
 QY 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 540
 DB 531 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 590
 QY 541 TTTTACCCTCCATGCTGCTGTTAAAGGAGAGATGGGAGCATCATTTCTGTTATATCTCTGTA 600
 DB 591 TTTTACCCTCCATGCTGCTGTTAAAGGAGAGATGGGAGCATCATTTCTGTTATATCTCTGTA 650
 QY 601 CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTCCATAGTGGAGAGCTTGTCTTCAG 660
 DB 651 CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTCCATAGTGGAGAGCTTGTCTTCAG 710
 QY 661 AACATAGGAGATGAAGTAAAGTGTCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
 DB 711 AACATAGGAGATGAAGTAAAGTGTCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 770
 QY 721 AGTTATTTTAG 780
 DB 771 AGTTATTTTAG 830
 QY 781 TGTGTGTGTATGCTGT 840
 DB 831 TGT 890
 QY 841 AGCCATTTCTAAGAGCTTGTATGTTTATGAGGCTGTGACTAGGATGATGATTTTCACGAAGGCA 900
 DB 891 AGCCATTTCTAAGAGCTTGTATGTTTATGAGGCTGTGACTAGGATGATGATTTTCACGAAGGCA 950
 QY 901 AGATTGGCATATCATTTGTAACATAAAAGCTGACATTTGACCCAGACATATTTGTAATCTTTT 960
 DB 951 AGATTGGCATATCATTTGTAACATAAAAGCTGACATTTGACCCAGACATATTTGTAATCTTTT 1010
 QY 961 CTAAAAATATATATATATATGCTTAACAGAAAGAGAGAACCGTTCTGTTGCAATCTACAG 1020
 DB 1011 CTAAAAATATATATATATGCTTAACAGAAAGAGAGAACCGTTCTGTTGCAATCTACAG 1070
 QY 1021 CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTTTCCAGAGTGTTCAGAGCCAAAGC 1080
 DB 1071 CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTTTCCAGAGTGTTCAGAGCCAAAGC 1130
 QY 1081 AAGAAGTTCAAGTGTCTTAGACAGAGGACATTAAGTATCATGTCTCTCTTTTAACTAGCATTA 1140
 DB 1131 AAGAAGTTCAAGTGTCTTAGACAGAGGACATTAAGTATCATGTCTCTCTTTTAACTAGCATTA 1190
 QY 1141 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGCATTAAGTCATTTCCATCAGCCAACT 1200
 DB 1191 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGCATTAAGTCATTTCCATCAGCCAACT 1250
 QY 1201 AAGTTGTCTCTTTTCTGTTTCTGTTTCCACATGGAACTTTTGTATTATAGTTAATCTTTC 1260
 DB 1251 AAGTTGTCTCTTTTCTGTTTCTGTTTCCACATGGAACTTTTGTATTATAGTTAATCTTTC 1310
 QY 1261 TATCTTGAATCTT 1273
 DB 1311 TATCTTGAATCTT 1323
 RESULT 3
 AAA54034
 ID AAA54034 standard; DNA; 2775 BP.
 XX
 AC AAA54034;
 XX
 XX 08-FEB-2001 (first entry)
 DT Human factor IX coding sequence.
 XX
 DE Vitamin K dependent protein; VKDP; gamma-carboxylation; chimeric protein;
 XX fusion protein; coagulation factor; Factor X; Factor VII; Protein S;
 KW Factor IX; Protein C; prothrombin; blood clotting; haemophilia; human;
 KW da.

XX OS Homo sapiens.
XX PN WO200054787-A1.
XX PD 21-SEP-2000.
XX PF 16-MAR-2000; 2000WO-US006934.
XX PR 16-MAR-1999; 99US-0124609P.
XX PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI High KA, Camire RM, Larson PJ, Stafford DW;
XX WI WI; 2000-638152/61.
XX PT Chimeric DNA for optimizing gamma carboxylation of vitamin K-dependent
PT protein useful for treating diseases associated with the protein,
PT comprises sequence encoding propeptide fused to sequence encoding the
PT protein.
XX PS Disclosure; Fig 6Di-ii; 60pp; English.
XX CC Efficient processing and release of mature two-chain factor X into the
CC circulation requires: removal of the signal sequence; formation of
CC disulfide bonds; modification of amino terminal glutamic acid residues,
CC to gamma-carboxyglutamic acid; modification of one aspartic acid in the
CC first epidermal growth factor (EGF) domain to Beta-hydroxyaspartic acid;
CC addition of N- and O-linked oligosaccharides to the activation peptide;
CC removal of an internal tripeptide to yield two-chain factor X and removal
CC of the propeptide just prior to secretion. While some of these
CC modifications do not appear essential for factor X function the removal
CC of the signal sequence, propeptide, internal tripeptide and full gamma-
CC carboxylation are all steps which are important requisites for the
CC production of biologically active factor X/FXa. Isolated chimeric
CC polynucleotides are described which encode a propeptide fused to a
CC nucleic acid sequence encoding a vitamin K-dependent protein (VKDP). The
CC fusion proteins encoded are vitamin K-dependent protein gamma-
CC carboxylation enhancers and are useful for optimising the gamma-
CC carboxylation of a VKDP to produce a fully gamma-carboxylated VKDP. The
CC fusion proteins and recombinant cells expressing them are useful for
CC alleviating a VKDP associated disease. The fusion constructs result in
CC the production of fully gamma-carboxylated mature VKDPs, which are
CC biologically active. The invention encompasses all combinations of
CC propeptide sequences (modified or not) and VKDP's. This sequence encodes
CC the signal, propeptide and mature protein sequence of human Factor IX
XX Sequence 2775 BP; 859 A; 528 C; 564 G; 824 T; 0 U; 0 Other;
Query Match 100.0%; Score 1273; DB 3; Length 2775;
Best Local Similarity 100.0%; Pred. No. 8.2e-279;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTCTCACTAACTCACTTTCCCATCTTTGTTAGATTTGAATATATACATCTAT 60
DB 1435 GGCTCTCACTAACTCACTTTCCCATCTTTGTTAGATTTGAATATATACATCTAT 1494
QY 61 GATCATTGCTTTTCTTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTCATTA 120
DB 1495 GATCATTGCTTTTCTTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTCATTA 1554
QY 121 GAAATGGACACNCTAGAGAAATATATGTTTGGAAATACAGTCATTTCTAAGGGCC 180
DB 1555 GAAATGGACACNCTAGAGAAATATATGTTTGGAAATACAGTCATTTCTAAGGGCC 1614
QY 181 CAGCCCTTGACAAAATTTGTAAGTAAATTTCTCCACTCTGTCATCAGATCTATGGTTC 240
DB 1615 CAGCCCTTGACAAAATTTGTAAGTAAATTTCTCCACTCTGTCATCAGATCTATGGTTC 1674
QY 241 TCCACTATGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCTCCCGAT 300

DB 1675 TCCACTATGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCTCCTCCGAT 1734
QY 301 CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTTCTGTATACAGTACAGGATC 360
DB 1735 CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTTCTGTATACAGTACAGGATC 1794
QY 361 TTTGGTCTACTCTATCACAAGGCCAGTACCACTCATGAAGAAAGAACACAGAGGATGAGC 420
DB 1795 TTTGGTCTACTCTATCACAAGGCCAGTACCACTCATGAAGAAAGAACACAGAGGATGAGC 1854
QY 421 TGAGAGGCTAAAACCTCATCAAAAACACATCTCTTTTCTCTACCTATTCCTCAATCTT 480
DB 1855 TGAGAGGCTAAAACCTCATCAAAAACACATCTCTTTTCTCTACCTATTCCTCAATCTT 1914
QY 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 540
DB 1915 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 1974
QY 541 TTTTACCCTCCATGTCGTTAAAGGAGAGATGGGGAGCATCATCTGTTTACTTCTCTGTA 600
DB 1975 TTTTACCCTCCATGTCGTTAAAGGAGAGATGGGGAGCATCATCTGTTTACTTCTGTA 2034
QY 601 CACAGTTATACATGTCATCAAAACCCAGACTTGTCTTCCATAGTGAGAGACTTGTCTTTCAG 660
DB 2035 CACAGTTATACATGTCATCAAAACCCAGACTTGTCTTCCATAGTGAGAGACTTGTCTTTCAG 2094
QY 661 AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 720
DB 2095 AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTT 2154
QY 721 AAGTTATTTTATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 780
DB 2155 AAGTTATTTTATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2214
QY 781 TGTGTGTGTATGCTGT 840
DB 2215 TGT 2274
QY 841 AGCCATTTCTAAGAGCTTGT 900
DB 2275 AGCCATTTCTAAGAGCTTGT 2334
QY 901 AGATTGGCATATCATTTGTAACCTTAAAGAGCTTGAACCTTGAACCTTGAACCTTGAACCT 960
DB 2335 AGATTGGCATATCATTTGTAACCTTAAAGAGCTTGAACCTTGAACCTTGAACCTTGAACCT 2394
QY 961 CTAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1020
DB 2395 CTAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2454
QY 1021 CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAAGC 1080
DB 2455 CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAAGC 2514
QY 1081 AAGAAGTTTGAAGTTTCCCTTAGACGAGGACATAGTATCATGTCTCTTTTAACTAGCATTA 1140
DB 2515 AAGAAGTTTGAAGTTTCCCTTAGACGAGGACATAGTATCATGTCTCTCTTTTAACTAGCATTA 2574
QY 1141 CCCCAGAGTGGAGAGGGTGCAGAGGCTCAAGAGCATTAAGTCAATTCCTCAATCAGGCAACT 1200
DB 2575 CCCCAGAGTGGAGAGGGTGCAGAGGCTCAAGAGCATTAAGTCAATTCCTCAATCAGGCAACT 2634
QY 1201 AAGTTGTCCTTTTCTGGTTTCTGGTTTCTGGTTTCTGGTTTCTGGTTTCTGGTTTCTGGTTT 1260
DB 2635 AAGTTGTCCTTTTCTGGTTTCTGGTTTCTGGTTTCTGGTTTCTGGTTTCTGGTTTCTGGTTT 2694
QY 1261 TATCTTGAATCTT 1273
DB 2695 TATCTTGAATCTT 2707
RESULT 4
ABV77053

ID AAF54018 standard; DNA; 38059 BP.
XX AAF54018;
XX
XX 30-MAR-2001 (first entry)
XX Human factor IX (hFIX) gene, SEQ ID NO:4.
XX
XX Age-related gene regulation; liver-specific; gene expression;
KW human factor IX; hFIX; AE5'; AE3'; age-regulatable expression construct;
KW antisense therapy; gene therapy; thrombosis; cardiovascular disease;
KW diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;
KW osteoarthritis; dementia; ds.
XX Homo sapiens.
XX WO200075279-A2.
PN
XX 14-DEC-2000.
PD
XX 06-JUN-2000; 2000WO-US015728.
PF
XX
XX 09-JUN-1999; 99US-00328925.
PR
XX (UNMI) UNIV MICHIGAN.
XX Kurachi K, Kurachi S;
XX
XX WPI; 2001-061708/07.
DR P-PSDB; AAB60281, AAB60282, AAB60283, AAB60284, AAB60285, AAB60286,
DR AAB60287, AAB60288, AAB60289.
XX
XX New regulatory elements that control age-related gene expression, useful
PT in gene therapy and for reducing Factor IX expression.
PT
XX
XX Disclosure; Fig 8A-E; 225pp; English.
XX
XX The invention relates to nucleic acid sequences which regulate gene
CC expression in an age-related manner and/or in a liver-specific manner.
CC The invention identifies regions of the human factor IX (hFIX) gene, and
CC a region of the human protein C (hPC) gene, which are age-related
CC regulatory sequences. The hFIX age-related regulatory sequences are
CC designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'
CC UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34393-
CC 35655 of AAF54018) respectively. These elements act synergistically to
CC increase hFIX levels over the lifespan of an individual; however, they
CC can independently exert effects on hFIX mRNA in an age-related manner,
CC with AE5' acting to stabilize hFIX mRNA, and AE3' acting to increase hFIX
CC mRNA levels, over time. AE5' also directs liver-specific expression. The
CC hPC gene age-related regulatory sequence is found in the 5' UTR
CC (AAF54081), and contains two PEA-3 (polyoma virus activator 3) elements
CC (5'-GAGGANA-3' and 5'-CAGGNAAG-3'. The age-related regulatory sequences of
CC the invention, along with their homologues, variants and fragments, may
CC be used in the construction of recombinant expression vectors for the
CC expression of a desired sequence in an age-related fashion in a host
CC cell. Preferred target genes for expression in such age-regulatable
CC expression vectors include those encoding proteins involved in blood
CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
CC anti-coagulants protein C and antithrombin III), human alpha-1-
CC antitrypsin, PEA-3 protein and reporter proteins such as luciferase.
CC Preferred promoters for use in such age-regulatable expression vectors
CC include the human factor IX promoter, the T7 promoter, the T3 promoter
CC and the SP6 promoter. The expression vectors of the invention may be used
CC in gene therapy to provide age- related and/or liver-specific expression
CC of target genes. Age-regulatable constructs may be used in the treatment
CC of such age-related conditions such as thrombosis, cardiovascular
CC disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,
CC osteoporosis, osteoarthritis and dementia. Specifically, they may be used
CC to express factor IX antisense mRNA in the treatment of thrombotic
CC conditions associated with the natural age-related rise in factor IX
CC expression. Transgenic cells or animals that contain vectors of the
CC invention are useful as models of these diseases, in screening for
CC potential therapeutic agents and for studying normal processes such as

CC	ageing and gene expression. Fragments and homologues of age-related
CC	regulatory sequences, are useful as probes to detect, isolate or identify
CC	other such sequences in samples. The present sequence represents the hFIX
CC	gene
XX	
SQ	Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1273; DB 4; Length 38059;
	Best Local Similarity 100.0%; Pred. No. 1.6e-278;
	Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GGCCTCTCACTAACTAACTACCTTTCCCATCTTTTGTAGATTGTAATATATACATTTCTAT 60
DB	
DB	34383 GGCCTCTCACTAACTAACTACCTTTCCCATCTTTTGTAGATTGTAATATATACATTTCTAT 34442
QY	61 GATCAATGCTTTTCTCTTTTACAGGGGAGAATTTTCATATTTTACCTGAGCAAAATGATTA 120
DB	
DB	34443 GATCAATGCTTTTCTCTTTTACAGGGGAGAATTTTCATATTTTACCTGAGCAAAATGATTA 34502
QY	121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCAATTTCTAAGGGCC 180
DB	
DB	34503 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCAATTTCTAAGGGCC 34562
QY	181 CAGCCCTTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 240
DB	
DB	34563 CAGCCCTTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 34622
QY	241 TCCACTATGGCAACTAATCACTCAATTTTCCCTCTTTAGCAGCAATCCATCTTCCCGAT 300
DB	
DB	34623 TCCACTATGGCAACTAATCACTCAATTTTCCCTCTTTAGCAGCAATCCATCTTCCCGAT 34682
QY	301 CTTCTTTTCTCTCCAAACCAATCATCAATGTTTATTAGTTTCTGTATACAGTACAGGATC 360
DB	
DB	34683 CTTCTTTTCTCTCCAAACCAATCATCAATGTTTATTAGTTTCTGTATACAGTACAGGATC 34742
QY	361 TTTTGTCTACTCTATCAACAGGCCAGTACCACTCATGAAGAAAGAACACAGAGTAGC 420
DB	
DB	34743 TTTTGTCTACTCTATCAACAGGCCAGTACCACTCATGAAGAAAGAACACAGAGTAGC 34802
QY	421 TGAGAGGCTAAACCTCATCAAAAAACATPACTCTTTTCTCTACCCCTATTCCTCAATCTT 480
DB	
DB	34803 TGAGAGGCTAAACCTCATCAAAAAACATPACTCTTTTCTCTACCCCTATTCCTCAATCTT 34862
QY	481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 540
DB	
DB	34863 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 34922
QY	541 TTTTACCCTCCATGGTCCGTTAAAGGAGAGATGGGGAGCATCATCTGTATTACTTCTGTA 600
DB	
DB	34923 TTTTACCCTCCATGGTCCGTTAAAGGAGAGATGGGGAGCATCATCTGTATTACTTCTGTA 34982
QY	601 CACAGTTATACATGCTTATCAAAACCCAGACTTGTCTTCCATAGTGAGACTTGTCTTTTCAG 660
DB	
DB	34983 CACAGTTATACATGCTTATCAAAACCCAGACTTGTCTTCCATAGTGAGACTTGTCTTTTCAG 35042
QY	661 AACATAGGATCAAGTAGGTCCTGAAAGCTTTGGGGGAAAGTTTCTTTCAGAGAGTT 720
DB	
DB	35043 AACATAGGATCAAGTAGGTCCTGAAAGCTTTGGGGGAAAGTTTCTTTCAGAGAGTT 35102
QY	721 AAGTTATTTTATATATAATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 780
DB	
DB	35103 AAGTTATTTTATATATAATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 35162
QY	781 TGTGTGTGTATGCGTGTGTGTAGACACACACACACACACATATATATATATATATATATAT 840
DB	
DB	35163 TGTGTGTGTATGCGTGTGTGTAGACACACACACACACACATATATATATATATATATATATAT 35222
QY	841 AGCCATTTCTAGAGCTTGTATGGTTATCGAGGCTCTGACTAGGCATGATTTTCCAGAGGCA 900
DB	
DB	35223 AGCCATTTCTAGAGCTTGTATGGTTATCGAGGCTCTGACTAGGCATGATTTTCCAGAGGCA 35282
QY	901 AGATTGGCATATCATTTGTTAACTAAAAAGCTGACATTCGACCCAGACATATTTGTACTCTTT 960
DB	

Db	35283	AGATTGGCATATCATTTGTAACTTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT	35342
Qy	961	CTAAAAATAATAATAATGCTTAAACAGAAAGAGAACCGTTCGTTTGGCAATCTACAG	1020
Db	35343	CTAAAAATAATAATAATGCTTAAACAGAAAGAGAACCGTTCGTTTGGCAATCTACAG	35402
Qy	1021	CTAGTAGAGACTTTGAGGAAGAAATTCACACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAAGC	1080
Db	35403	CTAGTAGAGACTTTGAGGAAGAAATTCACACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAAGC	35462
Qy	1081	AAGAAGTTGGAAGTTGCTTACACAGAGGACATTAAGTATCATGTCTCCTTTAACTAGCATATA	1140
Db	35463	AAGAAGTTGGAAGTTGCTTACACAGAGGACATTAAGTATCATGTCTCCTTTAACTAGCATATA	35522
Qy	1141	CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAAGTCATTCCAAATCAGGCCAACT	1200
Db	35523	CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAAGTCATTCCAAATCAGGCCAACT	35582
Qy	1201	AAGTTGTCCTTTTCTCGTTTCGTGTTCCACCATGGAACATTTTGTATTAGTAAATCCTTC	1260
Db	35583	AAGTTGTCCTTTTCTCGTTTCGTGTTCCACCATGGAACATTTTGTATTAGTAAATCCTTC	35642
Qy	1261	TATCTTGAATCTTT	1273
Db	35643	TATCTTGAATCTTT	35655

RESULT 6

RESOL 6
ABN95627

ID ABN95627 standard; DNA: 38059 BP.

[illegible]

AC ABN95627;

1. **XX**

DT 13-AUG-2002 (first entry)

XX

DE Gene #2125 used to diagnose liver cancer.

XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.

XX

OS Homo sapiens.

XX

PN WO200229103-A2.

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PD 11-APR-2002.

[illegible]

PF 02-OCT-2001; 2001WO-US030589.

XX

PR 02-OCT-2000; 2000US-0237054P.
yy

XX
PA (GENE-) GENE LOGIC INC

PA (GENE-) GENE LOGIC INC.
XX

PT Horne D. Alvares C. peregrina-silva s. Vockley J.C.

FI ROHNE U, ALVARES C, PERES-DA-SILVA S, VOCKLEY JG, XX

WPI: 2002-426119/45.

XX
XX
:C4/CTT074-2007, T3M YG

Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.

PS Claim 1; SEQ ID NO 2125; 298pp; English.

[illegible]

The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as

Db 35283 AGATTGGCATATCATTTGTAACATAAAAGCTGACATTGACCCAGACATATTTGTAATCTTT 35342
Qy 961 CTAAAAATATATATATATCTTAACAGAAAGAGAGACCGTTGCTTTGCAATCTACAG 1020
Db 35343 CTAAAAATATATATATATCTTAACAGAAAGAGAGACCGTTGCTTTGCAATCTACAG 35402
Qy 1021 CTAGTAGAGACTTTGAGGAGAAATTCACAGTGTGTCTTCCAGCAGTGTTCAGAGCCAAGC 1080
Db 35403 CTAGTAGAGACTTTGAGGAGAAATTCACAGTGTGTCTTCCAGCAGTGTTCAGAGCCAAGC 35462
Qy 1081 AAGAAGTTGAAGTTGCTAGACAGAGGACATATATCTCTCTTTAACTAGCATTA 1140
Db 35463 AAGAAGTTGAAGTTGCTAGACAGAGGACATATATCTCTCTTTAACTAGCATTA 35522
Qy 1141 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGACATAGTCATTCGAATCAGCCAAT 1200
Db 35523 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGACATAGTCATTCGAATCAGCCAAT 35582
Qy 1201 AAGTTCTCTCTTTCTGTTTCCGTTTCCACATGGAACATTTTGATTATATAGTTTAACTCTTC 1260
Db 35583 AAGTTCTCTCTTTCTGTTTCCGTTTCCACATGGAACATTTTGATTATATAGTTTAACTCTTC 35642
Qy 1261 TATCTTGAATCTT 1273
Db 35643 TATCTTGAATCTT 35655
RESULT 7
ID ADD71098 standard; DNA; 38059 BP.
XX ADD71098;
AC ADD71098;
XX 15-JAN-2004 (first entry)
DT Human coagulation factor IX gene SEQ ID NO:102.
DE liver cancer; chronic hepatitis; cirrhosis; liver disease; hepatotropic;
KW cytostatic; gene therapy; human; gene; ds.
XX Homo sapiens.
XX WO2003061564-A2.
XX 31-JUL-2003.
XX 20-DEC-2002; 2002WO-US040718.
XX 21-DEC-2001; 2001US-0341815P.
XX 31-DEC-2001; 2001US-0343185P.
XX (GENE-) GENE LOGIC INC.
PA (LGBI-) LG BIOMEDICAL INST.
XX Koh SS, Liu Q, Chung H, Zeng W, Lee B, Yeramilli S, Song SY;
XX WPI; 2003-663343/62.
XX Diagnosing liver cancer cells, useful for treating liver cancer
PT associated with chronic hepatitis or cirrhosis comprises detecting the
PT level of expression in a tissue sample of one or more genes associated
PT with cancerous liver tissues.
XX Claim 1; SEQ ID NO 102; 176pp; English.
XX The present invention describes a method for diagnosing liver cancer
CC cells comprising detecting the level of expression in a tissue sample of
CC one or more genes given in the specification (see ADD70997 to ADD71105),
CC where differential expression of the genes is indicative of liver cancer.
CC Also described: (1) detecting the progression of liver cancer in a
CC patient; (2) monitoring the treatment of a patient with liver cancer; (3)
CC treating a patient with liver cancer; (4) typing a liver disease in a

CC patient; (5) detecting the presence or progression of liver cancer in a
CC patient with chronic hepatitis or cirrhosis; (6) differentiating liver
CC cancer related to chronic hepatitis from liver cancer related to
CC cirrhosis; (7) screening for an agent capable of modulating the onset or
CC progression of liver cancer; (8) a composition comprising at least two
CC oligonucleotides comprising a sequence that specifically hybridizes to
CC any of the genes; (9) a solid support comprising the at least two
CC oligonucleotides; (10) a computer system comprising a database containing
CC information identifying the level in liver tissue of a set of genes; (11)
CC a method for using the computer system to present information identifying
CC the expression level in tissue or cell of any of the genes; and (12) a
CC therapeutic agent for slowing or halting the progression of liver cancer.
CC The methods are useful for treating liver cancer associated with chronic
CC hepatitis or cirrhosis. The present sequence represents a specifically
CC claimed human gene sequence which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other;
Query Match 100.0%; Score 1273; DB 10; Length 38059;
Best Local Similarity 100.0%; Pred. No. 1.6e-278; Indels 0; Gaps 0;
Matches 1273; Conservative 0; Mismatches 0;
Qy 1 GGCCTCTCACAATACTACCTTTCCCATCTTTTGTAGATTGAATATATATCTAT 60
Db 34383 GGCCTCTCACAATACTACCTTTCCCATCTTTTGTAGATTGAATATATATCTAT 34442
Qy 61 GATCATTTGCTTTTCTTTTACAGGGGAGAAATTCATATTTTACCTGAGCAATGATT 120
Db 34443 GATCATTTGCTTTTCTTTTACAGGGGAGAAATTCATATTTTACCTGAGCAATGATT 34502
Qy 121 GAAATGGAAACCACTAGAGGAAATAATGTGTAGAAATACAGTCATTTCTAAGGGCC 180
Db 34503 GAAATGGAAACCACTAGAGGAAATAATGTGTAGAAATACAGTCATTTCTAAGGGCC 34562
Qy 181 CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 240
Db 34563 CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGTTTC 34622
Qy 241 TCCACTATGGGAACCTAACTCACTCAATTTTCCCTCTTACAGAGCATTCATCTCCGAT 300
Db 34623 TCCACTATGGGAACCTAACTCACTCAATTTTCCCTCTTACAGAGCATTCATCTCCGAT 34682
Qy 301 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATAGTTCTGTATACAGTACAGGATC 360
Db 34683 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATAGTTCTGTATACAGTACAGGATC 34742
Qy 361 TTTGGTCTACTCTATCACAAGGCCAGTACACACTCATGAAGAAAGAAACACAGGAGTAGC 420
Db 34743 TTTGGTCTACTCTATCACAAGGCCAGTACACACTCATGAAGAAAGAAACACAGGAGTAGC 34802
Qy 421 TGAGAGGCTAAACCTCATCAAAAACACTACTCTTTTCTCTACCTATTCCTCAATCTT 480
Db 34803 TGAGAGGCTAAACCTCATCAAAAACACTACTCTTTTCTCTACCTATTCCTCAATCTT 34862
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC 540
Db 34863 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC 34922
Qy 541 TTTTACCCTTCCATGCTGTTTAAAGGAGAGATGGGAGCATCTCTGTTTATATCTTCTGTA 600
Db 34923 TTTTACCCTTCCATGCTGTTTAAAGGAGAGATGGGAGCATCTCTGTTTATATCTTCTGTA 34982
Qy 601 CACAGTTATACATGTCTATCAAAACCCAGACTTGTCTTCCATAGTGAGAGCTTCTTTTCAG 660
Db 34983 CACAGTTATACATGTCTATCAAAACCCAGACTTGTCTTCCATAGTGAGAGCTTCTTTTCAG 35042
Qy 661 AACATAGGAGTCAAGTAAAGTCCCTGAAAAGTTTGGGGAAAAGTTTCTTTTCAGAGATT 720
Db 35043 AACATAGGAGTCAAGTAAAGTCCCTGAAAAGTTTGGGGAAAAGTTTCTTTTCAGAGATT 35102
Qy 721 AAGTTATTTTAG 780
Db AAGTTATTTTAG 780

Db 301 TTCTTTGCTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCT 360
Qy 362 TTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTAGCT 421
Db 361 TTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTAGCT 420
Qy 422 GAGAGGCTAAACTCATCAAAACACTACTCCTTTTCTCTACCCCTATTCCCTCAATCTTTT 481
Db 421 GAGAGGCTAAACTCATCAAAACACTACTCCTTTTCTCTACCCCTATTCCCTCAATCTTTT 480
Qy 482 TACCTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTTCTTTTCTTTTCTCTCTCTCTCTCT 541
Db 481 TACCTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTTTCTTTTCTTTTCTCTCTCTCTCT 540
Qy 542 TTTACCTCTCATGGTGGTTAAAGGAGAGATGGGAGCATCTCTGTTTACTTCTGTATC 601
Db 541 TTTACCTCTCATGGTGGTTAAAGGAGAGATGGGAGCATCTCTGTTTACTTCTGTATC 600
Qy 602 ACAGTTATACATGCTCTATCAAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTTCAGA 661
Db 601 ACAGTTATACATGCTCTATCAAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTTCAGA 660
Qy 662 ACATAGGATGAAGTAAAGTGCTGAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTTA 721
Db 661 ACATAGGATGAAGTAAAGTGCTGAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTTA 720
Qy 722 AGTTATTTTAGT 781
Db 721 AGTTATTTTAGT 780
Qy 782 GTGTGTGCTGTATGCTGTGTAGACACACACACATACACATATATATATATATATATATAT 841
Db 781 GTGTGTGCTGTATGCTGTGTAGACACACACACATACACATATATATATATATATATATAT 840
Qy 842 GCCATTCTAAGAGCTTGTATGTTATGAGGCTGTGATAGGATGATATTTTCAGAGGCA 901
Db 841 GCCATTCTAAGAGCTTGTATGTTATGAGGCTGTGATAGGATGATATTTTCAGAGGCA 900
Qy 902 GATTGGCATATCATTTGTAATAAAGCTGACATTTGACCCAGACATATTTGACTCTTTTC 961
Db 901 GATTGGCATATCATTTGTAATAAAGCTGACATTTGACCCAGACATATTTGACTCTTTTC 960
Qy 962 TAAATAAT 1021
Db 961 TAAATAAT 1020
Qy 1022 TAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCCAAGCA 1081
Db 1021 TAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCCAAGCA 1080
Qy 1082 AGAAGTTGAAGTTGCTTAGACAGGACATATAGTATCATGCTCTCTTTAAGTATAGCATAC 1141
Db 1081 AGAAGTTGAAGTTGCTTAGACAGGACATATAGTATCATGCTCTCTTTAAGTATAGCATAC 1140
Qy 1142 CCCGAAGTGGAGAGGTCAGCAGGCTCAAGGCAATAGTCAATCCCAATCAGCCCAACTA 1201
Db 1141 CCCGAAGTGGAGAGGTCAGCAGGCTCAAGGCAATAGTCAATCCCAATCAGCCCAACTA 1200
Qy 1202 AGTTGTCCTTTTCTGTTTCTGTTTCCATGATGATGATGATGATGATGATGATGATGATGAT 1261
Db 1201 AGTTGTCCTTTTCTGTTTCTGTTTCCATGATGATGATGATGATGATGATGATGATGATGAT 1260
Qy 1262 ATCTTGAATCTT 1273
Db 1261 ATCTTGAATCTT 1272

RESULT 9
AAFS4074
ID AAF54074 standard; DNA; 1273 BP.
XX
AC AAF54074;
XX

DT 30-MAR-2001 (first entry)
DE hFIX gene AE3' age-related regulatory region homologue, SEQ ID NO:77.
XX
KW Age-related gene regulation; gene expression; human factor IX; hFIX;
AE3'; 3' UTR; 3' untranslated region; AE3'; element;
KW age-regulatable expression construct; antisense therapy; gene therapy;
thrombosis; cardiovascular disease; diabetes; Alzheimer's disease;
KW Parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200075279-A2.
XX 14-DEC-2000.
XX 06-JUN-2000; 2000WO-US015728.
XX 09-JUN-1999; 99US-00328925.
XX (UNMI) UNIV MICHIGAN.
XX Kurachi K, Kurachi S;
XX WPI; 2001-061708/07.
XX
XX New regulatory elements that control age-related gene expression, useful
in gene therapy and for reducing Factor IX expression.
XX
XX Disclosure; Fig 3B; 225pp; English.
XX
XX The invention relates to nucleic acid sequences which regulate gene
expression in an age-related manner and/or in a liver-specific manner.
XX The invention identifies regions of the human factor IX (hFIX) gene, and
XX a region of the human protein C (hPC) gene, which are age-related
XX regulatory sequences. The hFIX age-related regulatory sequences are
XX designated AE3' (AAFS4016) and AE3' (AAFS4017) and are found in the 5'
XX UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34383-
XX 35655 of AAF54018) respectively. These elements act synergistically to
XX increase hFIX levels over the lifespan of an individual; however, they
XX can independently exert effects on hFIX mRNA in an age-related manner,
XX with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX
XX mRNA levels, over time. AE5' also directs liver-specific expression. The
XX hPC gene age-related regulatory sequence is found in the 5' UTR
XX (AAFS4081), and contains two PEA-3 (polyoma virus activator 3) elements
XX 5'-GAGGAAA-3' and 5'-CAGGAA-3'. The age-related regulatory sequences of
XX the invention, along with their homologues, variants and fragments, may
XX be used in the construction of recombinant expression vectors for the
XX expression of a desired sequence in an age-related fashion in a host
XX cell. Preferred target genes for expression in such age-regulatable
XX expression vectors include those encoding proteins involved in blood
XX coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
XX anti-coagulants protein C and antithrombin III), human alpha-1-
XX antitrypsin, PEA-3 protein and reporter proteins such as luciferase.
XX Preferred promoters for use in such age-regulatable expression vectors
XX include the human factor IX promoter, the T7 promoter, the T3 promoter
XX and the SP6 promoter. The expression vectors of the invention may be used
XX in gene therapy to provide age- related and/or liver-specific expression
XX of target genes. Age-regulatable constructs may be used in the treatment
XX of such age-related conditions such as thrombosis, cardiovascular
XX disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,
XX osteoporosis, osteoarthritis and dementia. Specifically, they may be used
XX to express factor IX antisense mRNA in the treatment of thrombotic
XX conditions associated with the natural age-related rise in factor IX
XX expression. Transgenic cells or animals that contain vectors of the
XX invention are useful as models of these diseases, in screening for
XX potential therapeutic agents and for studying normal processes such as
XX ageing and gene expression. Fragments and homologues of age-related
XX regulatory sequences, are useful as probes to detect, isolate or identify
XX other such sequences in samples. The present sequence represents an AE3'
XX region homologue

SQ		Sequence	1273 BP; 393 A; 263 C; 217 G; 400 T; 0 U; 0 Other;
Query Match		99.9%; Score 1271.4; DB 4; Length 1273;	
Best Local Similarity		99.9%; Pred. No. 1.6e-278;	
Matches 1272; Conservative		0; Mismatches 1; Indels 0; Gaps 0;	
QY	1	GGCCTCTCACTAATCACTTTCCCATCTTTTGGTAGATTTGAATATATACATTCAT	60
DB	1	GGCCTCTCACTAATCACTTTCCCATCTTTTGGTAGATTTGAATATATACATTCAT	60
QY	61	GATCATTTGCTTTTCTCTTTACAGGGAGAAATTTCAATTTTACCTGAGCAAAATGATTA	120
DB	61	GATCATTTGCTTTTCTCTTTACAGGGAGAAATTTCAATTTTACCTGAGCAAAATGATTA	120
QY	121	GAATAATGGAACCACTAGAGGAATATAATGTGTGTAGGAAATATACAGTCATTTCTAAGGGCC	180
DB	121	GAATAATGGAACCACTAGAGGAATATAATGTGTGTAGGAAATATACAGTCATTTCTAAGGGCC	180
QY	181	CAGCCCTTGACAAAATGTGAAGTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC	240
DB	181	CAGCCCTTGACAAAATGTGAAGTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC	240
QY	241	TCCACTATGCAACTCACTCACTCAATTTTCCCTCCTTAGCAGCATTTCCATCTCCCGAT	300
DB	241	TCCACTATGCAACTCACTCACTCAATTTTCCCTCCTTAGCAGCATTTCCATCTCCCGAT	300
QY	301	CTTCTTTGCTTTCTCCAAACCAACATCAATGTTTATTTAGTTCTGTATACAGTACAGGATC	360
DB	301	CTTCTTTGCTTTCTCCAAACCAACATCAATGTTTATTTAGTTCTGTATACAGTACAGGATC	360
QY	361	TTTGGTCTACTCTATCAAGGCGAGTACCACTCATGAAAGAAAGAACACAGGAGTAGC	420
DB	361	TTTGGTCTACTCTATCAAGGCGAGTACCACTCATGAAAGAAAGAACACAGGAGTAGC	420
QY	421	TGAGAGCTTAAACTCATCAAAACACTACTCTTTTCTCTACCCCTATTCCTCAATCTT	480
DB	421	TGAGAGCTTAAACTCATCAAAACACTACTCTTTTCTCTACCCCTATTCCTCAATCTT	480
QY	481	TTACCTTTTCCAAATCCCAATCCCAATTCAGTCTTTCTTTTACTCCCTCTCTCCC	540
DB	481	TTACCTTTTCCAAATCCCAATCCCAATTCAGTCTTTCTTTTACTCCCTCTCTCCC	540
QY	541	TTTTACCTCCATGCTGTTTAAAGGAGAGATGGGAGCATCATTTCTGTTATATCTTCTGTA	600
DB	541	TTTTACCTCCATGCTGTTTAAAGGAGAGATGGGAGCATCATTTCTGTTATATCTTCTGTA	600
QY	601	CACAGTTATACATGCTATCAAAACCCAGACTTCTCCATAGTGGAGACTTGCTTTTCAG	660
DB	601	CACAGTTATACATGCTATCAAAACCCAGACTTCTCCATAGTGGAGACTTGCTTTTCAG	660
QY	661	AACATAGGGATGAAGTGAAGTGCTGCTGAAAGTTTGGGGGAAAGTTTCTTTTCAGAGATT	720
DB	661	AACATAGGGATGAAGTGAAGTGCTGCTGAAAGTTTGGGGGAAAGTTTCTTTTCAGAGATT	720
QY	721	AAGTTATTTTAG	780
DB	721	AAGTTATTTTAG	780
QY	781	TGTGTGTGTATGCTGT	840
DB	781	TGTGTGTGTGTATGCTGT	840
QY	841	AGCCATTTCTAAGAGCTTGTATGTTTATGAGGCTCTAGGAGTATGATTTTCAGAGGCA	900
DB	841	AGCCATTTCTAAGAGCTTGTATGTTTATGAGGCTCTAGGAGTATGATTTTCAGAGGCA	900
QY	901	AGATTGGCATATCATTTGTAACCTAAATAAGCTGACATTGACCCAGACATATTTGACTCTTT	960
DB	901	AGATTGGCATATCATTTGTAACCTAAATAAGCTGACATTGACCCAGACATATTTGACTCTTT	960
QY	961	CTAAAAATACAG	1020
DB	961	CTAAAAATACAG	1020

QY	1021	CTAGTAGAGACTTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCCAAGC	1080
DB	1021	CTAGTAGAGACTTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCCAAGC	1080
QY	1081	AAGAAAGTTGAAGTTGCTCTAGACCAGAGGACATTAAGTATATCATGTCTCTCTTAACCTAGCATA	1140
DB	1081	AAGAAAGTTGAAGTTGCTCTAGACCAGAGGACATTAAGTATATCATGTCTCTCTTAACCTAGCATA	1140
QY	1141	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAGGACATAGTCAATTCACCAATCAGCCAACT	1200
DB	1141	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAGGACATAGTCAATTCACCAATCAGCCAACT	1200
QY	1201	AAGTTGTCTCTTTTCTCGTTTCGTTTCCACCATGGAACATTTTCAATTATAGTTAATCTCTTC	1260
DB	1201	AAGTTGTCTCTTTTCTCGTTTCGTTTCCACCATGGAACATTTTCAATTATAGTTAATCTCTTC	1260
QY	1261	TATCTTTGAATCTTT 1273	
DB	1261	TATCTTTGAATCTTT 1273	

RESULT 10
AAF54073
ID AAF54073 standard; DNA; 1273 BP.
XX
XX AAF54073;
XX AC
XX
DT 30-MAR-2001 (first entry)
XX
DE hFIX gene AE3' age-related regulatory region homologue, SEQ ID NO:76.
XX
KW Age-related gene regulation; gene expression; human factor IX; hFIX;
KW AE3'; 3' UTR; 3' untranslated region; AE3' element;
KW age-regulatable expression construct; antisense therapy; gene therapy;
KW thrombosis; cardiovascular disease; diabetes; Alzheimer's disease;
KW Parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN W0200075279-A2.
XX
PD 14-DEC-2000.
XX
PF 06-JUN-2000; 2000WO-US015728.
XX
PR 09-JUN-1999; 99US-00328925.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Kurachi K, Kurachi S;
XX
DR WPI; 2001-061708/07.
XX
PT New regulatory elements that control age-related gene expression, useful
PT in gene therapy and for reducing Factor IX expression.
XX
PS Disclosure; Fig 3A; 225pp; English.
XX
CC The invention relates to nucleic acid sequences which regulate gene
CC expression in an age-related manner and/or in a liver-specific manner.
CC The invention identifies regions of the human factor IX (hFIX) gene, and
CC a region of the human protein C (hPC) gene, which are age-related
CC regulatory sequences. The hFIX age-related regulatory sequences are
CC designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'
CC UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34383-
CC 35655 of AAF54018) respectively. These elements act synergistically to
CC increase hFIX levels over the lifespan of an individual; however, they
CC can independently exert effects on hFIX mRNA in an age-related manner,
CC with AE5' acting to stabilize hFIX mRNA, and AE3' acting to increase hFIX
CC mRNA levels, over time. AE5' also directs liver-specific expression. The
CC hPC gene age-related regulatory sequence is found in the 5' UTR

CC (AAF54081), and contains two PBA-3 (polyoma virus activator 3) elements
CC 5'-GAGGAAA-3' and 5'-CAGGAAG-3'. The age-related regulatory sequences of
CC the invention, along with their homologues, variants and fragments, may
CC be used in the construction of recombinant expression vectors for the
CC expression of a desired sequence in an age-related fashion in a host
CC cell. Preferred target genes for expression in such age-regulatable
CC expression vectors include those encoding proteins involved in blood
CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
CC anti-coagulants protein C and antithrombin III), human alpha-1-
CC antitrypsin, PEA-3 protein and reporter proteins such as luciferase.
CC Preferred promoters for use in such age-regulatable expression vectors
CC include the human factor IX promoter, the T7 promoter, the T3 promoter
CC and the SP6 promoter. The expression vectors of the invention may be used
CC in gene therapy to provide age-related and/or liver-specific expression
CC of target genes. Age-regulatable constructs may be used in the treatment
CC of such age-related conditions such as thrombosis, cardiovascular
CC disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,
CC osteoporosis, osteoarthritis and dementia. Specifically, they may be used
CC to express factor IX antisense mRNA in the treatment of thrombotic
CC conditions associated with the natural age-related rise in factor IX
CC expression. Transgenic cells or animals that contain vectors of the
CC invention are useful as models of these diseases, in screening for
CC potential therapeutic agents and for studying normal processes such as
CC ageing and gene expression. Fragments and homologues of age-related
CC regulatory sequences, are useful as probes to detect, isolate or identify
CC other such sequences in samples. The present sequence represents an AE3'
CC region homologue

XX SQ Sequence 1273 BP; 392 A; 262 C; 218 G; 401 T; 0 U; 0 Other;

Query Match 99.9%; Score 1271.4; DB 4; Length 1273;
Best Local Similarity 99.9%; Pred. No. 1.6e-278;
Matches 1272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCTCTCACTAACTCACTTCCCATCTTTTGTAGATTGGAATATATACATCTAT 60
DB 1 GGCCTCTGACTAACTAACTCACTTCCCATCTTTTGTAGATTGGAATATATACATCTAT 60
QY 61 GATCATTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA 120
DB 61 GATCATTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA 120
QY 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTTTAAAGGGCC 180
DB 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTTTAAAGGGCC 180
QY 181 CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACATGTTTC 240
DB 181 CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACATGTTTC 240
QY 241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTTACAGCAGCATTCCTCCGAT 300
DB 241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTTACAGCAGCATTCCTCCGAT 300
QY 301 CTTCTTTGTCTTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
DB 301 CTTCTTTGTCTTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
QY 361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAGAACACAGGAGTAGC 420
DB 361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAGAACACAGGAGTAGC 420
QY 421 TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTTCTTACCTCTATTCCTCAATCTT 480
DB 421 TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTTCTTACCTCTATTCCTCAATCTT 480
QY 481 TTACCTTTTCCAAATCCCAATCCCAATCCAGTTTCTTTTCTTCTTCTCTCTCTCC 540
DB 481 TTACCTTTTCCAAATCCCAATCCCAATCCAGTTTCTTTCTTCTTCTCTCTCTCC 540
QY 541 TTTTACCCCTCCATGGTGGTAAAGGAGAGATGGGGAGCATCATCTGTTATACTCTGTA 600
DB 541 TTTTACCCCTCCATGGTGGTAAAGGAGAGATGGGGAGCATCATCTGTTATACTCTGTA 600

QY 601 CACAGTTATACATGCTATCAAAACCAGACTTGCTTCCATAGTGAGACTTCTCTTTTCAG 660
DB 601 CACAGTTATACATGCTATCAAAACCAGACTTGCTTCCATAGTGAGACTTCTCTTTTCAG 660
QY 661 AACATAGGATGAAGTAAAGTGCCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
DB 661 AACATAGGATGAAGTAAAGTGCCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
QY 721 AAGTTATTTTATATATATAATATATATAATAATAATAATAATAATAATAATAATAATA 780
DB 721 AAGTTATTTTATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 780
QY 781 TGTGTGTGTGTATGCGTGTGTAGACACACACGATACACATATATATGAAGCAATA 840
DB 781 TGTGTGTGTGTATGCGTGTGTAGACACACACGATACACATATATATGAAGCAATA 840
QY 841 AGCCATTCTTAAGAGCTTGTATGGGTTATGGAGTCTGACTAGGCATGATTTCAAGAGGCA 900
DB 841 AGCCATTCTTAAGAGCTTGTATGGGTTATGGAGTCTGACTAGGCATGATTTCAAGAGGCA 900
QY 901 AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTGCCAGACATATTTGTAATCTTT 960
DB 901 AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTGCCAGACATATTTGTAATCTTT 960
QY 961 CTAAAAATAATAATAATAATGCTAAACAGAAAGAGAACCGTTTGGTTGCAATCTACAG 1020
DB 961 CTAAAAATAATAATAATAATGCTAAACAGAAAGAGAACCGTTTGGTTGCAATCTACAG 1020
QY 1021 CTAGTAGAGACTTTTCAAGGAAGAAATTCACAGTGTCTTTCAGCAGTGTTCAGAGGCAAGC 1080
DB 1021 CTAGTAGAGACTTTTCAAGGAAGAAATTCACAGTGTCTTTCAGCAGTGTTCAGAGGCAAGC 1080
QY 1081 AAGAAGTTGAAGTTCCCTAGACAGGACATTAAGTATCATGCTCTCTTTTAACTAGCATA 1140
DB 1081 AAGAAGTTGAAGTTCCCTAGACAGGACATTAAGTATCATGCTCTCTCTTTTAACTAGCATA 1140
QY 1141 CCCCAGCTGGAGAGGGTGCAGCAGGCTCAAGGCAATAGTCATTCCCAATCAGGCAACT 1200
DB 1141 CCCCAGCTGGAGAGGGTGCAGCAGGCTCAAGGCAATAGTCATTCCCAATCAGGCAACT 1200
QY 1201 AAGTTGTCTCTTTCTGGTTTCTGTTTCCCATGGAACATTTTGTATAGTTAATCTCTTC 1260
DB 1201 AAGTTGTCTCTTTCTGGTTTCTGTTTCCCATGGAACATTTTGTATAGTTAATCTCTTC 1260
QY 1261 TATCTTGAATCTT 1273
DB 1261 TATCTTGAATCTT 1273

RESULT 11

AAF54075

ID AAF54075 standard; DNA; 1273 BP.

XX AC AAF54075;

XX DT 30-MAR-2001 (first entry)

XX DE hFIX gene AE3' age-related regulatory region homologue, SEQ ID NO:78.

XX KW Age-related gene regulation; gene expression; human factor IX; hFIX;

XX KW AE3'; 3' UTR; 3' untranslated region; AE3' element;

XX KW age-regulatable expression construct; antisense therapy; gene therapy;

XX KW thrombosis; cardiovascular disease; diabetes; Alzheimer's disease;

XX KW Parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia; ds.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200075279-A2.

XX PD 14-DEC-2000.

XX XX

PF 06-JUN-2000; 2000WO-US015728.
 PR 09-JUN-1999; 99US-00328925.
 XX (UNMI) UNIV MICHIGAN.
 XX Kurachi K, Kurachi S;
 PI WPI; 2001-061708/07.
 XX
 PT New regulatory elements that control age-related gene expression, useful
 PT in gene therapy and for reducing Factor IX expression.
 XX
 XX Disclosure; Fig 3B; 225pp; English.
 CC The invention relates to nucleic acid sequences which regulate gene
 CC expression in an age-related manner and/or in a liver-specific manner.
 CC The invention identifies regions of the human factor IX (hFIX) gene, and
 CC a region of the human protein C (hpc) gene, which are age-related
 CC regulatory sequences. The hFIX age-related regulatory sequences are
 CC designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'
 CC UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34383-
 CC 35655 of AAF54018) respectively. These elements act synergistically to
 CC increase hFIX levels over the lifespan of an individual; however, they
 CC can independently exert effects on hFIX mRNA in an age-related manner,
 CC with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX
 CC mRNA levels, over time. AE5' also directs liver-specific expression. The
 CC hpc gene age-related regulatory sequence is found in the 5' UTR
 CC (AAF54081), and contains two PEA-3 (polyoma virus activator 3) elements
 CC (5'-GAGGAAA-3' and 5'-CAGGAG-3'. The age-related regulatory sequences of
 CC the invention, along with their homologues, variants and fragments, may
 CC be used in the construction of recombinant expression vectors for the
 CC expression of a desired sequence in an age-related fashion in a host
 CC cell. Preferred target genes for expression in such age-regulatable
 CC expression vectors include those encoding proteins involved in blood
 CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
 CC anti-coagulants protein C and antithrombin III), human alpha-1-
 CC antitrypsin, PEA-3 protein and reporter proteins such as luciferase.
 CC Preferred promoters for use in such age-regulatable expression vectors
 CC include the human factor IX promoter, the T7 promoter, the T3 promoter
 CC and the SP6 promoter. The expression vectors of the invention may be used
 CC in gene therapy to provide age- related and/or liver-specific expression
 CC of target genes. Age-regulatable constructs may be used in the treatment
 CC of such age-related conditions such as thrombosis, cardiovascular
 CC disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer,
 CC osteoporosis, osteoarthritis and dementia. Specifically, they may be used
 CC to express factor IX antisense mRNA in the treatment of thrombotic
 CC conditions associated with the natural age-related rise in factor IX
 CC expression. Transgenic cells or animals that contain vectors of the
 CC invention are useful as models of these diseases, in screening for
 CC potential therapeutic agents and for studying normal processes such as
 CC ageing and gene expression. Fragments and homologues of age-related
 CC regulatory sequences, are useful as probes to detect, isolate or identify
 CC other such sequences in samples. The present sequence represents an AE3'
 CC region homologue
 XX
 SQ Sequence 1273 BP; 392 A; 263 C; 217 G; 401 T; 0 U; 0 Other;
 Query Match 99.7%; Score 1269.8; DB 4; Length 1273;
 Best Local Similarity 99.8%; Pred. No. 3.6e-278;
 Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GGCTCTCACTAACTACATCTCCCATCTTTGTTAGATTGGAATATATACATTTCTAT 60
 DB 1 GGCTCTCACTAACTAACTCTTCCCATCTTTGTTAGATTGGAATATATACATTTCTAT 60
 QY 61 GATCATTTGTTTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTCATTA 120
 DB 61 GATCATTTGTTTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTCATTA 120
 QY 121 GAAATGGAAACCACTAGAGGAATATAATGTTGTAGGAAATACAGTCATTTCTAAGGGCC 180
 DB 121 GAAATGGAAACCACTAGAGGAATATAATGTTGTAGGAAATACAGTCATTTCTAAGGGCC 180

181 CAGCCCTTGACAAAAATTGGAAGTTAAATTTCTCCACTCTCTCCATCAGATACTATGTTTC 240
 181 CAGCCCTTGACAAAAATTGGAAGTTAAATTTCTCCACTCTCTCCATCAGATACTATGTTTC 240
 241 TCCACTATGGCAAACTAACTCACTCAATTTTCCCTCTCTTAGCAGCATTTCCATCTTCCCGAT 300
 241 TCCACTATGGCAAACTAACTCACTCAATTTTCCCTCTCTTAGCAGCATTTCCATCTTCCCGAT 300
 301 CTTCTTTGCTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGATC 360
 301 CTTCTTTGCTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGATC 360
 361 TTTGGTCTACTCTATCAAGGCCAGTACCACTCATGAAGAAAGAACACAGAGTAGC 420
 361 TTTGGTCTACTCTATCAAGGCCAGTACCACTCATGAAGAAAGAACACAGAGTAGC 420
 421 TGAGAGGCTTAAACTCATCAAAAACACTACTCTTTTCTCTTACCTTATTCCTCAATCTT 480
 421 TGAGAGGCTTAAACTCATCAAAAACACTACTCTTTTCTCTTACCTTATTCCTCAATCTT 480
 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 540
 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 540
 541 TTTTACCCTCCATGGTCTGTTAAAGAGAGATGGGAGAGCATCATTTCTGTATATCTTCTGTA 600
 541 TTTTACCCTCCATGGTCTGTTAAAGAGAGATGGGAGAGCATCATTTCTGTATATCTTCTGTA 600
 601 CACAGTTATACATGCTCTATCAAAACCAGACTTCTCTTCCATAGTGGAGAGCTTGTCTTTTTCAG 660
 601 CACAGTTATACATGCTCTATCAAAACCAGACTTCTCTTCCATAGTGGAGAGCTTGTCTTTTTCAG 660
 661 AACATAGGATGAAGTAAAGTCTGCTCAAAAGTTTGGGGGAAAGATTTCTTTTCAGAGATT 720
 661 AACATAGGATGAAGTAAAGTCTGCTCAAAAGTTTGGGGGAAAGATTTCTTTTCAGAGATT 720
 721 AAGTTATTTTATATATATATATATATAATAATATATATAATAATAATAATAATAATAATA 780
 721 AAGTTATTTTATATATATATATATATAATAATAATAATAATAATAATAATAATAATAATA 780
 781 TGTGTGTGTATGCTGT 840
 781 TGTGTGTGTGTATGCTGT 840
 841 AGCCATTCTAAGAGCTTGTATGTTTATGAGGCTGTGACTAGGATGATTTTTCAGAGGCA 900
 841 AGCCATTCTAAGAGCTTGTATGTTTATGAGGCTGTGACTAGGATGATTTTTCAGAGGCA 900
 901 AGATTGGCATATCATTTGTAACCTTAAAGGCTGACATTTGACCCAGACATATTGTACTCTTT 960
 901 AGATTGGCATATCATTTGTAACCTTAAAGGCTGACATTTGACCCAGACATATTGTACTCTTT 960
 961 CTAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1020
 961 CTAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1020
 1021 CTAGTAGACATTTGAGGAGAAATTTCAACAGTGTGTCTTTTCAGAGGCTTTCAGAGCCAGC 1080
 1021 CTAGTAGACATTTGAGGAGAAATTTCAACAGTGTGTCTTTTCAGAGGCTTTCAGAGCCAGC 1080
 1081 AAGAGTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTTAACTAGCATA 1140
 1081 AAGAGTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTTAACTAGCATA 1140
 1141 CCCCCAAGTGGAGAGGGTGCAGCAGGCTCAAAGGCATTAAGTCATTTCCAAATCAGCAACT 1200
 1141 CCCCCAAGTGGAGAGGGTGCAGCAGGCTCAAAGGCATTAAGTCATTTCCAAATCAGCAACT 1200
 1201 AAGTTGTCTCTTTCTGTTTCTGTTTCCACATGGAAATTTGATTTATATAGTTAATCTTTC 1260
 1201 AAGTTGTCTCTTTCTGTTTCTGTTTCCACATGGAAATTTGATTTATATAGTTAATCTTTC 1260

Qy	1261	TATCTTGAATCTT	1273
Dd	1261		1273
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RESULT 12			
AAZ8626			
ID	AAZ8626 standard; DNA; 2792 BP.		
XX	AC	AAZ8626;	
XX	07-JUN-1999	(first entry)	
DE	Nucleotide sequence of human factor IX-R338A.		
XX			
KW	Human, Factor IX-R338A; substitution; Factor X; Factor Ya;		
KW	mammalian blood coagulation cascade; phospholipid surface; calcium ion;		
KW	Factor VIIla; Blood clotting; haemophilia B; ss.		
OS	Homo sapiens.		
OS	Synthetic.		
Key	Location/Qualifiers		
FT	CDS	/56..1423	
FT	/*tag= a		
FT	/product= "Factor IX-R338A"		
PX	WO9903496-A1.		
XX	28-JAN-1999.		
XX	17-JUL-1998;	98WO-US014750.	
PF	21-JUL-1997;	97US-0053571P.	
PR	(UYNC-) UNIV NORTH CAROLINA.		
PA	(STAF/) STAFFORD D W.		
PA	(CHAN/) CHANG J L.		
PI	Stafford DW, Chang JL;		
XX	WPI; 1999-131867/11.		
DR	P-PSDB; AAY03203.		
PT	Factor IX antihemophilic factor with increased clotting activity - due to		
PT	an amino acid substitution (of arginine) at position 338.		
XX	Disclosure; Page 26-32; 38pp; English.		
CC	This is the nucleotide sequence encoding a non-naturally occurring human		
CC	Factor IX-R338A protein having an amino acid substitution at amino acid		
CC	position 338 of arginine to alanine. Factor IX converts Factor X to		
CC	Factor Xa in the mammalian blood coagulation cascade, in a process that		
CC	requires a phospholipid surface, calcium ions and Factor VIIla. Nucleic		
CC	acids encoding Factor IX can be used to facilitate blood clotting, e.g.		
CC	in patients afflicted with haemophilia B		
XX	Sequence 2792 BP; 858 A; 541 C; 569 G; 824 T; 0 U; 0 Other;		
SQ			
<hr/>			
Query Match 99.7%; Score 1269.8; DB 2; Length 2792;			
Best Local Similarity 99.8%; Pred. No. 4.4e-278;			
Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	1	GGCCTCTCACTAACACTTCCTCCCATCTTTGTTAGATTGTAATATACATTTCTAT	60
Dd	1452	GGCCTCTCACTAACACTTCCTCCCATCTTTGTTAGATTGTAATATACATTTCTAT	1511
<hr/>			
Qy	61	GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTTCATATTTTACCCTGAGCAAATTGATTA	120
Dd	1512	GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTTCATATTTTACCCTGAGCAAATTGATTA	1571
<hr/>			
Qy	121	AAAAATGGAACCACTAGAGGAATAATGTGTAGGAAAATTACAGTCAATTTCTTAAGGCC	180

Db 2544 AAGAAGUUGAAGUUGCCUAGACACAGAGGACAUAGUAUCAUGUUCUUUAUACUAGCAUA 2603

Qy 1141 CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAAAGGCATAGTCAATCCATCAGCCAACT 1200

Db 2604 CCCCGAAGUAGAGGGUCCAGCAGGCUCAAGGCAUAGUACUCCAAUACGACCAUCU 2663

Qy 1201 AAGTTGCTCTTCTGTTGTTGTTGCACATCGAACAATTTGATTATGTTAATCCTTC 1260

Db 2664 AAGUUGUCCUUCUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUG 2723

Qy 1261 TATCTTGAATCTT 1273

Db 2724 UAUUGUUAUUCU 2736

RESULT 15

AAF54076

ID AAF54076 standard; DNA; 1273 BP.

XX AAF54076;

XX 30-MAR-2001 (first entry)

XX hFIX gene AE3' age-related regulatory region homologue, SEQ ID NO:79.

XX Age-related gene regulation; gene expression; human factor IX; hFIX;

KW AE3'; 3' UTR; 3' untranslated region; AE3'; element;

KW age-regulatable expression construct; antisense therapy; gene therapy;

KW thrombosis; cardiovascular disease; diabetes; Alzheimer's disease;

KW Parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia; ds.

XX Homo sapiens.

OS Synthetic.

XX WO200075279-A2.

XX 14-DEC-2000.

XX 06-JUN-2000; 2000WO-US015728.

XX 09-JUN-1999; 99US-00328925.

XX (UNMI) UNIV MITCHIGAN.

XX Kurachi K, Kurachi S;

XX WPI; 2001-061708/07.

XX New regulatory elements that control age-related gene expression, useful

PT in gene therapy and for reducing Factor IX expression.

XX Disclosure; Fig 3C; 225pp; English.

PS

CC The invention relates to nucleic acid sequences which regulate gene

CC expression in an age-related manner and/or in a liver-specific manner.

CC The invention identifies regions of the human factor IX (hFIX) gene, and

CC a region of the human protein C (hPC) gene, which are age-related

CC regulatory sequences. The hFIX age-related regulatory sequences are

CC designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'

CC UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position 34383-

CC 35655 of AAF54018) respectively. These elements act synergistically to

CC increase hFIX levels over the lifespan of an individual; however, they

CC can independently exert effects on hFIX mRNA in an age-related manner.

CC with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX

CC mRNA levels, over time. AE5' also directs liver-specific expression. The

CC hPC gene age-related regulatory sequence is found in the 5' UTR

CC (AAF54081), and contains two PEA-3 (polyoma virus activator 3) elements

CC 5'-GAGGAAA-3' and 5'-CAGGAAG-3'. The age-related regulatory sequences

CC the invention, along with their homologues, variants and fragments, may

CC be used in the construction of recombinant expression vectors for the

CC expression of a desired sequence in an age-related fashion in a host

CC cell. Preferred target genes for expression in such age-regulatable

CC expression vectors include those encoding proteins involved in blood

CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the

CC anti-coagulants protein C and antithrombin III), human alpha-1-

CC antitrypsin, PEA-3 protein and reporter proteins such as luciferase.

CC Preferred promoters for use in such age-regulatable expression vectors

CC include the human factor IX promoter, the T7 promoter, the T3 promoter

CC and the SP6 promoter. The expression vectors of the invention may be used

CC in gene therapy to provide age-related and/or liver-specific expression

CC of target genes. Age-regulatable constructs may be used in the treatment

CC of such age-related conditions such as thrombosis, cardiovascular

CC disease, diabetes, Alzheimer's disease, Parkinson's disease, cancer, and

CC osteoporosis, osteoarthritis and dementia. Specifically, they may be used

CC to express factor IX antisense mRNA in the treatment of thrombotic

CC conditions associated with the natural age-related rise in factor IX

CC expression. Transgenic cells or animals that contain vectors of the

CC invention are useful as models of these diseases, in screening for

CC potential therapeutic agents and for studying normal processes such as

CC ageing and gene expression. Fragments and homologues of age-related

CC regulatory sequences, are useful as probes to detect, isolate or identify

CC other such sequences in samples. The present sequence represents an AE3',

CC region homologue

XX

SQ Sequence 1273 BP; 392 A; 263 C; 217 G; 401 T; 0 U; 0 Other;

Query Match 99.5%; Score 1266; DB 4; Length 1273;

Best Local Similarity 99.7%; Pred. No. 1.9e-277;

Matches 1269; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGCCTCTCACTAACTAACTCCATCTTCCATCTTTGTTAGATTGAATATATACATCTAT 60

Db 1 GGCCTCTCACTAACTAACTCCATCTTCCATCTTTGTTAGATTGAATATATACATCTAT 60

Qy 61 GATCATTGCTTTTCTCTTTTACAGGGGAGAAATTTCAATATTTTACCTGAGCAAAATGATTA 120

Db 61 GATCATTGCTTTTCTCTTTTACAGGGGAGAAATTTCAATATTTTACCTGAGCAAAATGATTA 120

Qy 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTCTTAAGGGCC 180

Db 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTCTTAAGGGCC 180

Qy 181 CAGCCCTTCACAAAATTTGGAAGTTAAATTTGCTCACTCTGTCCATCAGATCTATGGTTC 240

Db 181 CAGCCCTTCACAAAATTTGGAAGTTAAATTTGCTCACTCTGTCCATCAGATCTATGGTTC 240

Qy 241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTCTAGCAGCATTTCCTCCGAT 300

Db 241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTCTAGCAGCATTTCCTCCGAT 300

Qy 301 CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Db 301 CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360

Qy 361 TTTGCTTACTCTATCACAAGGCCAGTACCACTCATGAAAGAAACACACAGGAGTAGC 420

Db 361 TTTGCTTACTCTATCACAAGGCCAGTACCACTCATGAAAGAAACACACAGGAGTAGC 420

Qy 421 TCAGAGGCTTAAACATCATCAAAAACACTACTCTTTTCTCTCTACCCCTTCTCTCAATCTT 480

Db 421 TCAGAGGCTTAAACATCATCAAAAACACTACTCTTTTCTCTCTACCCCTTCTCTCAATCTT 480

Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCTT 540

Db 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCTT 540

Qy 541 TTTTACCTTCCATGGTGTGTTAAAGGAGAGATGGGGAGCATCATCTGTGTATATCTTCTGTA 600

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 13:51:23 ; Search time 5457 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1273	100.0	1707	6	AX379348 Sequence
3	1273	100.0	2775	6	AR178034 Sequence
4	1273	100.0	2775	9	HUMCIX
5	1273	100.0	2775	11	G28615
6	1273	100.0	2804	6	CQ882048
7	1273	100.0	2804	6	AR452580
8	1273	100.0	38059	6	AR390767
9	1273	100.0	38059	6	AX409478
10	1273	100.0	38059	9	HUMFIXG
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13	1271.4	99.9	1273	6	AR390822
14	1271.4	99.9	35458	9	AF536327
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ALIGNMENTS

RESULT 1
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LOCUS AR390766 1273 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6610906.
ACCESSION AR390766
VERSION AR390766.1 GI:40113107
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1273)
AUTHORS Kurachi, K. and Kurachi, S.
TITLE Nucleotide sequences for gene regulation and methods of use thereof
JOURNAL Patent: US 6610906-A 3 26-AUG-2003;
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LOCUS AX379348 1707 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 7 from Patent WO0198482.
ACCESSION AX379348
VERSION AX379348.1 GI:19575188
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Miao,C.H. and Kay,M.A.
TITLE Liver-specific gene expression cassettes, and methods of use
JOURNAL Patent: WO 0198482-A 7 27-DEC-2001;
The Board of Trustees of The Leland Stanford Junior University (US)
; The University of Washington (US)
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.4e-261;
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LOCUS 2775 bp mRNA linear PRI 01-NOV-1994
DEFINITION Human coagulation factor IX mRNA, complete cds.
ACCESSION M11309
VERSION M11309.1 GI:180552
KEYWORDS clotting factor; clotting factor IX; coagulation factor;
coagulation factor IX; factor IX.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2775)
AUTHORS McGraw,R.A., Davis,L.M., Noyes,C.M., Lundblad,R.L., Roberts,H.R.,
Graham,J.B. and Stafford,D.W.
TITLE Evidence for a prevalent dimorphism in the activation peptide of
human coagulation factor IX
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 82 (9), 2847-2851 (1985)
MEDLINE 85190593
PUBMED 3857619
REFERENCE 2 (bases 214 to 222; 313 to 321; 877 to 885)
AUTHORS Chen,S.H., Thompson,A.R., Zhang,M. and Scott,C.R.
TITLE Three point mutations in the factor IX genes of five hemophilia B
patients. Identification strategy using localization by altered
epitopes in their hemophilic proteins
J. Clin. Invest. 84 (1), 113-118 (1989)

JOURNAL 89292150
MEDLINE 2472424
PUBMED
COMMENT Original source text: Human liver cdna to mRNA.
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Best Local Similarity 100.0%; Pred. No. 2.3e-261;
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DEFINITION	human STS SHGC-35785, sequence tagged site.		STS 11-JUL-1996
ACCESSION	G28615		
VERSION	G28615.1	GI:1408430	
KEYWORDS	STS; STS sequence; primer; sequence tagged site.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 2775)		
	Myers,R.M.		
	Unpublished (1996)		

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: GTAAGTGCTGAAAGTTTG
Primer B: GTGAAATCATGCCTAGTCAGACC
STS size: 219
PCR profile:

Line:	Initial incubation:	94 degrees C for 90 seconds
	Denaturation:	94 degrees C for 15 seconds
	Annealing:	62 degrees C for 23 seconds
	Polymerization:	72 degrees C for 30 seconds
	PCR Cycles:	30
	Thermal Cycler:	Perkin Elmer 9600

Protocol:									
Template:	25 ng								
Primer:	each 1 uM								
dNTPs:	each 200 uM								
Taq Polymerase:	0.05 units/ul								
Total Vol:	10 ul								
Buffer:									
MgCl2:	2.5 mM								
KCl:	50 mM								
Tris-HCl:	20 mM								
pH:	8.3								
Prepared with primer pairs provided by Sandoz, derived from M11309									
-- Washington University/Merck EST sequence.									
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STS	2109..2327								
primer_bind	2109..2130								
primer_bind	complement(2305..2327)								
ORIGIN									
Query Match	100.0%; Score 1273; DB 11; Length 2775;								
Best Local Similarity	100.0%; Pred. No. 2.3e-261;								
Matches 1273; Conservative	0; Mismatches 0; Indels 0; Gaps 0								
Qy	1	GGCCTCTCACTAACTACACTTTCCCACTCTTTTGGTAGATTTTGAATATATACATTCAT	60						
Db	1435	GGCCTCTCACTAACTAACTACTTTCCCACTCTTTTGGTAGATTTTGAATATATACATTCAT	149						
Qy	61	GATCAATTCCTTTTCTCTTTACAGGGGAGAAATTTTCATATTTTACTGAGCAAAATGATTA	120						
Db	1495	GATCAATTCCTTTTCTCTTTACAGGGGAGAAATTTTCATATTTTACTGAGCAAAATGATTA	155						
Qy	121	GAAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTTCTAAGGGCC	180						
Db	1555	GAAATGGAAACCACTAGAGGATATAATGTGTAGGAAATTTACAGTCATTTCTAAGGGCC	161						
Qy	181	CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC	240						
Db	1615	CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC	167						
Qy	241	TCCACTATGGCACTAACTCACTCAATTTTCTCCCTCTAGCAGCAATTCATCTTCCCGAT	300						
Db	1675	TCCAATAAGCACTAACTCACTCAATTTTCTCCCTCTAGCAGCAATTCATCTTCCCGAT	173						
Qy	301	CTTCTTTGCTTCTCCAAACCAACATCAATTTTATTTAGTTCTCTATACAGTACAGGATC	360						
Db	1735	CTTCTTTGCTTCTCCAAACCAACATCAATTTTATTTAGTTCTCTATACAGTACAGGATC	179						
Qy	361	TTTGGTCTACTCTATCAAGAGCCAGTACACACTCATGAAGAAGAACACAGGAGTAGC	420						
Db	1795	TTTGGTCTACTCTATCAAGAGCCAGTACCACTCATGAAGAAGAACACAGGAGTAGC	185						
Qy	421	TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTTCCCTCTACCCCTATTTCCCTCAATCTT	480						
Db	1855	TGAGAGGCTAAACCTCATCAAAAACACTACTCTCTTTTCCCTCTACCCCTATTTCCCTCAATCTT	191						
Qy	481	TTACTCTTTCCAAATCCCAATCCCAATCAGTTTTTCTCTTTCTACTCCCTCTCTCCC	540						
Db	1915	TTACTCTTTCCAAATCCCAATCCCAATCAGTTTTTCTCTTTCTACTCCCTCTCTCCC	197						
Qy	541	TTTTTACCCTCCATGGTCTGTAAAGGAGAGATGGGAGCATCATTTCTGTATACTTCTGTGA	600						
Db	1975	TTTTTACCCTCCATGGTCTGTAAAGGAGAGATGGGAGCATCATTTCTGTATACTTCTGTGA	203						
Qy	601	CACAGTTATACATGTCTPATCAAAACCCAGACTTGTCTCCATAGTGGAGACTTGTCTTTTCAG	660						
Db	2035	CACAGTTATACATGTCTPATCAAAACCCAGACTTGTCTCCATAGTGGAGACTTGTCTTTTCAG	209						

Db 2544 AAGAGTTGAAGTGGCTAGACAGAGGACATAGATCAATGCTCTCTTAACTAGCATTA 2603
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Qy 1201 AGTTGTCCTTTCTCGTTTCGTTTCACCATGGAACATTTTGAATATAGTAACTCTTC 1260
Db 2664 AAGTTGTCCTTTCTCGTTTCGTTTCACCATGGAACATTTTGAATATAGTAACTCTTC 2723
Qy 1261 TATCTTGAATCTT 1273
Db 2724 TATCTTGAATCTT 2736

RESULT 7
AR452580
LOCUS AR452580 2804 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2 from patent US 6677369.
ACCESSION AR452580
VERSION AR452580.1 GI:42684368
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2804)
AUTHORS Beight,D.W., Craft,T.J., Franciskovich,J.B., Goodson,T. Jr., Hall,S.E., Herron,D.K., Klinkowski,V.J., Masters,J.J., Mendel,D., Milst,G., Sawyer,J.S., Shuman,R.T., Smith,G.F., Tebbe,A.L., Tinsley,J.M., Weir,L.C., Wikel,J.H., Wiley,M.R. and Yee,Y.K.
TITLE Antithrombotic agents
JOURNAL Patent: US 6677369-A 2 13-JAN-2004;
FEATURES Location/Qualifiers
source 1..2804
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 1273; DB 6; Length 2804;
Best Local Similarity 100.0%; Pred. No. 2.3e-261;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTCTCACTAACTCACTTCCCATCTTTGTTAGATTGGAATATATACATCTAT 60
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Qy 61 GATCATTGCTTTTCTTTACAGGGAGAAATTCATATTTTACCTGAGCAATTCATTA 120
Db 1524 GATCATTGCTTTTCTTTACAGGGAGAAATTCATATTTTACCTGAGCAATTCATTA 1583
Qy 121 GAAATGGAACCACTAGAGGAATATAATGTTAGGAAATTTACAGTCATTTCTTAAGGGCC 180
Db 1584 GAAATGGAACCACTAGAGGAATATAATGTTAGGAAATTTACAGTCATTTCTTAAGGGCC 1643
Qy 181 CAGCCCTTGACAAAATTTGAGAGTAAATTCCTCACTCTGTCATCAGATCACTATGGTTC 240
Db 1644 CAGCCCTTGACAAAATTTGAGAGTAAATTCCTCACTCTGTCATCAGATCACTATGGTTC 1703
Qy 241 TCACATATGGCAACTAACTCACTCAATTTTCCCTCTTACGAGCAATTCATCTCCCGAT 300
Db 1704 TCACATATGGCAACTAACTCACTCAATTTTCCCTCTTACGAGCAATTCATCTCCCGAT 1763
Qy 301 CTTCCTTTGCTCTCCCAACCAACATCAATGTTTATTAGTCTGTATACAGTACAGGATC 360
Db 1764 CTTCCTTTGCTCTCCCAACCAACATCAATGTTTATTAGTCTGTATACAGTACAGGATC 1823
Qy 361 TTTGGTCTACTCTATCACAAGGCCAGTACCACTCATGAAGAAAGAACACAGGAGTAGC 420
Db 1824 TTTGGTCTACTCTATCACAAGGCCAGTACCACTCATGAAGAAAGAACACAGGAGTAGC 1883
Qy 421 TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTCTTACCCCTATTCCTCAATCTT 480

Db 1884 TGAGAGGCTAAAACTCATCAAAAACACTACTCTCTTTCTCTACCCCTATTCCTCAATCTT 1943
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 540
Db 1944 TTACCTTTTCCAAATCCCAATCCCAATCAGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 2003
Qy 541 TTTTACCCCTCCATGTCGTTTAAAGGAGAGATGGGAGCATCATCTCTGTTTACTTTCTGTA 600
Db 2004 TTTTACCCCTCCATGTCGTTTAAAGGAGAGATGGGAGCATCATCTCTGTTTACTTTCTGTA 2063
Qy 601 CACAGTTATACATGTCATCAAAACCCAGACTTGTCTCCATAGTGGAGACTTGTCTTTTCAG 660
Db 2064 CACAGTTATACATGTCATCAAAACCCAGACTTGTCTCCATAGTGGAGACTTGTCTTTTCAG 2123
Qy 661 AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTT 720
Db 2124 AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTT 2183
Qy 721 AAGTTATTTTAT 780
Db 2184 AAGTTATTTTAT 2243
Qy 781 TGTGTGTGTATGCGTGTGTGTAGACACACACGCGATACACATATATATATATATATATATAT 840
Db 2244 TGTGTGTGTATGCGTGTGTGTAGACACACACGCGATACACATATATATATATATATATAT 2303
Qy 841 AGCCATTCTAAGAGCTTTGTATGGTGTGTAGAGGTCTGACTAGGATGATTTTCACCAAGGCA 900
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Qy 1021 CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGGCCAAGC 1080
Db 2484 CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGGCCAAGC 2543
Qy 1081 AAGAAGTTGAAGTGCCTAGACAGGACATTAAGTATCATGTCTCTCTTTTAACTAGCATTA 1140
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Db 2604 CCCCAGAGTGGAGAGGGTGCAGCAGGCTCAAGGCATTAAGTCATTTCCAATCAGCCAACT 2663
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Db 2664 AAGTTGTCTCTTTCTGTTTTCGTTTTCACCATGGAACATTTTGGATTATAGTTAATCCTTC 2723
Qy 1261 TATCTTGAATCTT 1273
Db 2724 TATCTTGAATCTT 2736

RESULT 8
AR390767
LOCUS AR390767 3805 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 4 from patent US 6610906.
ACCESSION AR390767
VERSION AR390767.1 GI:40113109
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3805)
AUTHORS Kurachi,K. and Kurachi,S.
TITLE Nucleotide sequences for gene regulation and methods of use thereof
JOURNAL Patent: US 6610906-A 4 26-AUG-2003;

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source		1..38059		
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Query Match		100.0%;	Score 1273; DB 6; Length 38059;	
Best Local Similarity		100.0%;	Pred. No. 1.9e-261;	
Matches 1273; Conservative		0;	Mismatches 0; Indels 0; Gaps 0;	
Qy	1	GGCCTCTCACTAACTCACTTCCCATCTTTTGTAGATTGGAATATATACATCTCTAT 60		
Db	34383	GGCCTCTCACTAACTCACTTCCCATCTTTTGTAGATTGGAATATATACATCTCTAT 34442		
Qy	61	GATCATGTCTTTTCTCTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTA 120		
Db	34443	GATCATGTCTTTTCTCTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTA 34502		
Qy	121	GAAATGGAACCACTAGAGGAATATAATGTGTAGGAATTTACAGTCAATTTCTAAGGGCC 180		
Db	34503	GAAATGGAACCACTAGAGGAATATAATGTGTAGGAATTTACAGTCAATTTCTAAGGGCC 34562		
Qy	181	CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC 240		
Db	34563	CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTC 34622		
Qy	241	TCCACTATGGCAACTCACTCAATTTTCCCTCTTAGCAGCATTCCTCTCCCGAT 300		
Db	34623	TCCACTATGGCAACTCACTCAATTTTCCCTCTTAGCAGCATTCCTCTCCCGAT 34682		
Qy	301	CTTCTTTTGTCTTCCAAACCAACATCAATGTTTATTAGTCTGTATACAGTACAGGATC 360		
Db	34683	CTTCTTTTGTCTTCCAAACCAACATCAATGTTTATTAGTCTGTATACAGTACAGGATC 34742		
Qy	361	TTTGGTCTACTCTATCAAGGCCAGTACACACTCATGAAGAAAGAACACAGGAGTAGC 420		
Db	34743	TTTGGTCTACTCTATCAAGGCCAGTACACACTCATGAAGAAAGAACACAGGAGTAGC 34802		
Qy	421	TGAGAGGCTAAACTCATCAAAACACTACTCTCTTTTCTTACCTTACCTTATTCCTCAATCTT 480		
Db	34803	TGAGAGGCTAAACTCATCAAAACACTACTCTCTTTTCTTACCTTATTCCTCAATCTT 34862		
Qy	481	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC 540		
Db	34863	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC 34922		
Qy	541	TTTTACCTCCATGTGCGTTAAAGGAGAGATGGGAGACATCAATCTGTATATCTCTGTA 600		
Db	34923	TTTTACCTCCATGTGCGTTAAAGGAGAGATGGGAGACATCAATCTGTATATCTCTGTA 34982		
Qy	601	CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTCAG 660		
Db	34983	CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTCAG 35042		
Qy	661	AACATAGGAGTGAAGTGAAGTGCCTCAAAAGTTTGGGGAAAGTTTCTTTCAGAGATT 720		
Db	35043	AACATAGGAGTGAAGTGAAGTGCCTCAAAAGTTTGGGGAAAGTTTCTTTCAGAGATT 35102		
Qy	721	AAGTTATTTTATATATATATATAATAATAATATAATAATAATAATAATAATAATAATATAG 780		
Db	35103	AAGTTATTTTATATATATATATAATAATAATAATAATAATAATAATAATAATAATAATATAG 35162		
Qy	781	TGTGTGTGTATGCGTGTGTAGACACACAGCGCATACACATATATATGGAAGCAATA 840		
Db	35163	TGTGTGTGTATGCGTGTGTAGACACACAGCGCATACACATATATATGGAAGCAATA 35222		
Qy	841	AGCCATTCTAAGAGCTTGTATGTGTATGAGGTCTGACTAGGCAATGATTTTCAGAGGCA 900		
Db	35223	AGCCATTCTAAGAGCTTGTATGTGTATGAGGTCTGACTAGGCAATGATTTTCAGAGGCA 35282		
Qy	901	AGATTGGCATATCATTTGTAACATAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT 960		
Db	35283	AGATTGGCATATCATTTGTAACATAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT 35342		

Qy	961	CTAAAAATAATAATAATAATGCTAACAGAAAGAGAGAACCGTTTCGTTTGCAATCTACAG	1020
Db	35343	CTAAAAATAATAATAATAATGCTAACAGAAAGAGAGAACCGTTTCGTTTGCAATCTACAG	35402
Qy	1021	CTAGTAGAGACTTTTGAGGAAGAAATCAACAGTGTGTCTTTCAGCAGTGTTCAGAGCCCAAGC	1080
Db	35403	CTAGTAGAGACTTTTGAGGAAGAAATCAACAGTGTGTCTTTCAGCAGTGTTCAGAGCCCAAGC	35462
Qy	1081	AAGAGATTGAAGTTGCGCTAGACAGAGACATAGTATCATGTCTCTCTTTAACTAGGATA	1140
Db	35463	AAGAGATTGAAGTTGCGCTAGACAGAGACATAGTATCATGTCTCTCTTTAACTAGGATA	35522
Qy	1141	CCCCAAGTGGAGAGGGTGCAGCAGGCTCAAAGGCATAAGTCAATCCAAATCAGCCCAACT	1200
Db	35523	CCCCAAGTGGAGAGGGTGCAGCAGGCTCAAAGGCATAAGTCAATCCAAATCAGCCCAACT	35582
Qy	1201	AAGTGTCTCTTTTCTGTCTTCCATGCAAT	

QY	301	CTTCTTTGTTCTTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	360
Db	34683	CTTCTTTGTTCTTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	34742
QY	361	TTTGGTCTACTCTATCACAAGGCCAGTACACACTCATGAAGAAGAACACAGGAGTAGC	420
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QY	421	TGAGAGGCTAAACTCATCAAAAACACTACTCTTTCTCTACCCCTATTCTCTCAATCTT	480
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QY	481	TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTCTTTCTTCTCTCTCTCCC	540
Db	34863	TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTCTTTCTCTCTCTCCC	34922
QY	541	TTTTACCCTCCATGTCGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTTCTGA	600
Db	34923	TTTTACCCTCCATGTCGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTTCTGA	34982
QY	601	CACAGTTATACATGCTCTATCAAAACCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTCAG	660
Db	34983	CACAGTTATACATGCTCTATCAAAACCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTCAG	35042
QY	661	AACATAGGGATGAAGTAAAGTGCCTGAAAGTTTGGGGAAAGTTTCTTTCAGAGAGTT	720
Db	35043	AACATAGGGATGAAGTAAAGTGCCTGAAAGTTTGGGGAAAGTTTCTTTCAGAGAGTT	35102
QY	721	AGATTATTTTAG	780
Db	35103	AGATTATTTTAG	35162
QY	781	TGTGTGTGTATGCTGT	840
Db	35163	TGTGTGTGTATGCTGT	35222
QY	841	AGCCATTCTAAGAGCTTGTATGGTGTATGGAGTCTGACTAGGCGATGATTTCCAGGAGCA	900
Db	35223	AGCCATTCTAAGAGCTTGTATGGTGTATGGAGTCTGACTAGGCGATGATTTCCAGGAGCA	35282
QY	901	AGATTGGCATATCATTTGTAACATAAAGCTGACATGACCCAGACATATGTGACTCTTT	960
Db	35283	AGATTGGCATATCATTTGTAACATAAAGCTGACATGACCCAGACATATGTGACTCTTT	35342
QY	961	CTAAAATAATAG	1020
Db	35343	CTAAAATAATAG	35402
QY	1021	CTAGTAGAGACTTTGAGGAAGAAATTCACACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAGC	1080
Db	35403	CTAGTAGAGACTTTGAGGAAGAAATTCACACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAGC	35462
QY	1081	AAGAAGTTGAAGTTGCTAGACAGAGGACATAAGTATCATGTCTCTTTAACTAGCATATA	1140
Db	35463	AAGAAGTTGAAGTTGCTAGACAGAGGACATAAGTATCATGTCTCTTTAACTAGCATATA	35522
QY	1141	CCCCGAAGTGGAGAGGGTGCACAGGCTCAAGGATTAAGTCAATCCATCAGCCAATC	1200
Db	35523	CCCCGAAGTGGAGAGGGTGCACAGGCTCAAGGATTAAGTCAATCCATCAGCCAATC	35582
QY	1201	AAGTTGTCCTTTTCTGTTTCTGTTTCCCATGGAACATTTTGAATATAGTTAATCCTTC	1260
Db	35583	AAGTTGTCCTTTTCTGTTTCTGTTTCCCATGGAACATTTTGAATATAGTTAATCCTTC	35642
QY	1261	TATCTTGAATCTT 1273	
Db	35643	TATCTTGAATCTT 35655	
RESULT 10			
HUMFIXG			
LOCUS			

Human coagulation factor IX gene; complete cds.	
K02402	
K02402.1	GI:182612
Alu repeat; Christmas factor; KpnI repetitive sequence;	
antihemophilic factor B; factor IX; repeat region; simple	
repetitive sequence.	
Homo sapiens (human)	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
1 (bases 1 to 38059)	
Yoshitake,S., Schach,B.G., Foster,D.C., Davie,E.W. and Kurachi,K.	
Nucleotide sequence of the gene for human factor IX (antihemophilic	
factor B)	
Biochemistry 24 (14), 3736-3750 (1985)	
86000558	
2994716	
2 (bases 23487 to 23556)	
Rees,D.J., Rizza,C.R. and Brownlee,G.G.	
Haemophilia B caused by a point mutation in a donor splice junction	
Nature 316 (6029), 643-645 (1985)	
85296286	
4033760	
3 (bases 23378 to 23387)	
Graham,J.B., Ljahn,D.B., Lord,S.T., Kirshstein,J., Nilsson,I.M.,	
Wallmark,A., Ljung,R., Frazier,L.D., Ware,J.L., Lin,S.W.,	
Stafford,D.W. and Bosco,J.	
The Maimo polymorphism of coagulation factor IX, an immunologic	
polymorphism due to dimorphism of residue 148 that is in linkage	
disequilibrium with two other F.IX polymorphisms	
Am. J. Hum. Genet. 42 (4), 573-580 (1988)	
88161064	
2450455	
4 (sites)	
Hirosawa,S., Fahner,J.B., Salter,J.-P., Wu,C.-T., Lovrien,E. and	
Kurachi,K.	
Structural and functional basis of the developmental regulation of	
human factor IX gene: factor IX Leyden	
Unpublished (1990)	
Original source text: Homo sapiens (clone:	
FIX-lambda-[6,36,53,61].) (tissue library: T.Maniatis et al.) DNA;	
and Homo sapiens (clone: FIX-lambda-4243) DNA.	
Sequence for [1] kindly submitted on floppy by K.Kurachi,	
05-AUG-1985.	
[1] notes a potential TATA box (2939-2942) and polyadenylation	
signal (35701-35706); and notes two start codons (downstream of the	
start codon annotated below) that may be alternative and/or	
preferred starts for the factor IX prepropeptide. Several tracts	
of simple repetitive sequence are present [1], including regions	
with the potential for hairpin and/or Z-DNA formation. [1]	
describes six long open reading frames in the intron and on the	
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Location/Qualifiers	
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1..2596	
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2966..35722	
/gene="F9"	
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CDS	variation	14076..14079 /genes="F9" /notes="tcga in one allele; nnnn in another allele (loss of TaqI site); G00-119-900" /replaces="nnnn" 18165..20265 /rpt_family="KpnI" 20416 /genes="F9" /citation={4} /replaces="a" 20634..20762 /genes="F9" /notes="G00-119-900" /number=5 20763..23327 /genes="F9" /notes="G00-119-900" /number=5 23328..23530 /genes="F9" /notes="G00-119-900" /number=6 23387 /genes="F9" /notes="g in [1]; a in [3] Ala->Thr; G00-119-900" /replaces="a" 23387 /genes="F9" /notes="g in one allele; a in another allele" /replaces="a" 23531..33003 /genes="F9" /note="G00-119-900" /number=6 23531 /genes="F9" /notes="g in [1]; t in [2] (haemophilia patient); G00-119-900" /replaces="t" 24172..24475 /rpt_family="Alu" 25863..26091 /rpt_family="Alu" 31537..31809 /rpt_family="Alu" 33004..33118 /genes="F9" /notes="G00-119-900" /number=7 33119..33786 /genes="F9" /note="G00-119-900"
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	variation	
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	intron	
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sig_peptide	variation	
	mat_peptide	
	mat_peptide	
	intron	
	repeat_region	
	variation	
	exon	
	intron	
	exon	
	intron	
variation	variation	
	exon	
	intron	
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	variation	
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	intron	
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	variation	
intron	variation	
	exon	
	intron	
	variation	
	exon	
	intron	
	variation	
	exon	
	intron	
	variation	

QY	722	AGTTATTTTATATATAATATAATATAATATAATATAATATAATATAATATAATAGT	781
Db	721	AGTTATTTTATATATAATATAATATAATATAATATAATATAATATAATATAATAGT	780
QY	782	GTGTGTGTGTATGCGTGTGTGTAGACACACACGCAATATAATATGAAGCAATAA	841
Db	781	GTGTGTGTGTATGCGTGTGTGTAGACACACACGCAATATAATATGAAGCAATAA	840
QY	842	GCCATTCTAAGAGCTGTATGTTATGAGGCTGTGATAGGCAATGATTTTCAAGAGCA	901
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QY	902	GATTGGCATATCAATCTAATAAAGCTGACATTTGACCCAGACATATTTGACTCTTTC	961
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QY	962	TAAAAATAATAATAATATGCTTAACAGAAAGAGAGAACCGTTTCGTTTCAATCTACAGC	1021
Db	961	TAAAAATAATAATAATATGCTTAACAGAAAGAGAGAACCGTTTCGTTTCAATCTACAGC	1020
QY	1022	TAGTAGAGACTTTGAGGAAGAATTTCAACAGTGTGTCTTACGAGTGTTCAGAGCCAAAGCA	1081
Db	1021	TAGTAGAGACTTTGAGGAAGAATTTCAACAGTGTGTCTTACGAGTGTTCAGAGCCAAAGCA	1080
QY	1082	AGAAGTTGAAGTTGCTTAGACACAGAGACATAAGTATCATGTCTCTTTAACTAGCATAC	1141
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QY	1142	CCGGAAGTGAGAGGGTGCAGCAGGCTCAAAGGCATAAGTCAATCCATCAGCCAACTA	1201
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QY	1202	AGTTGTCTTTTCTGTGTGTGTGTGTTTCCATGGAACATTTTGAATATAGTTAATCTTCT	1261
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DEFINITION Sequence 76 from patent US 6610906.			
ACCESSION AR390821			
VERSION AR390821.1 GI:40113172			
KEYWORDS			
SOURCE Unknown.			
ORGANISM Unknown.			
REFERENCE 1 (bases 1 to 1273)			
AUTHORS Kurachi, K. and Kurachi, S.			
TITLE Nucleotide sequences for gene regulation and methods of use thereof			
JOURNAL Patent: US 6610906-A 76 26-AUG-2003;			
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Best Local Similarity 99.9%; Pred. No. 5.5e-261;			
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QY	61	GATCATGTCTTTTCTTTTACAGGGGAGAAATTTATATTTTACCTGAGCAAAATGATTA	120
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QY	121	GAAAATGGAAACCACTAGAGGAATATAATGTGTAGAAATTTACAGTCATTTCTAAGGGCC	180
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QY	181	CAGCCCTTTGACAAAAATTTGTGAAGTTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTTC	240
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ACCESSION	AR390823			
VERSION	AR390823.1	GI:40113174		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1. (bases 1 to 1273)			
AUTHORS	Kurachi, K. and Kurachi, S.			
TITLE	Nucleotide sequences for gene regulation and methods of use thereof			
JOURNAL	Patent: US 6610906-A 78 26-AUG-2003;			
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Best Local Similarity 99.8%; Pred. No. 1.2e-260; Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
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Qy	181	CAGCCCTTGACAAATTTGGAAGTTAAATCTCCACTCTGTCCATCAGATACATGGTTC	240
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Qy	661	AACATAGGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT	720
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Qy	841	AGCCATTTCTAAGAGCTTGTATGTTATGGAGGTCTGACTAGGCATGATTTCAAGAGGCA	900
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9	1271.4	99.9	36755	4	US-09-949-016-5252
10	1269.8	99.7	1273	4	US-09-328-925-78
11	1269.8	99.7	2792	4	US-09-118-748-1
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13	1266.6	99.5	1273	4	US-09-328-925-79
14	1261	99.1	1272	4	US-09-328-925-82
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17	1186.4	93.2	2340	3	US-08-742-877-3
18	110	8.6	1610	1	US-08-209-846A-6
19	110	8.6	1610	2	US-08-472-809B-6
20	110	8.6	1610	3	US-08-438-265-6
21	109	8.6	1548	1	US-08-106-078-15
22	109	8.6	1548	2	US-08-591-492-21
23	109	8.6	1548	2	US-08-484-891-6
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ALIGNMENTS

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; Sequence 3, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-925-3

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Best Local Similarity		100.0%	Pred. No. 0;		
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Db	1	GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTGTAGATTGTAATATATACATTCTAT	60		
Qy	61	GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTCATT	120		
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Qy	121	GAATATGGAACCACTAGAGGAATAATGTGTAGGAATTTACAGTCATTCTTAAGGGCC	180		
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Qy	181	CAGCCCTTGACAAAATTTGGAAGTTAAATCTTCCACTCTGTCCATCAGATACATATGGTTC	240		
Db	181	CAGCCCTTGACAAAATTTGGAAGTTAAATCTTCCACTCTGTCCATCAGATACATATGGTTC	240		
Qy	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCATTCCTCCCAT	300		
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Qy	301	CTTCTTTTGTCTTCCAAACCAAAACATCAATGTTTATTTAGTCTGTATACAGTACAGATC	360		
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RESULT 2

US-09-053-871A-22
; Sequence 22, Application US/09053871A
; Patent No. 6315995
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; APPLICANT: Stern, David
; APPLICANT: Rose, Eric
; APPLICANT: Solomon, Robert A.
; APPLICANT: Schmidt, Ann Marie

; TITLE OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING
; FILE OF INVENTION: STROKE OUTCOME
; CURRENT APPLICATION NUMBER: US/09/053.871A
; CURRENT FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2775
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-053-871A-22

Query Match 100.0%; Score 1273; DB 3; Length 2775;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCCTCTCACATAACTTAATCACTTTCCCATCTTTTGTAGATTGAAATATATACATTTCTAT 60
Db 1435 GGCCTCTCACATAACTTAATCACTTTCCCATCTTTTGTAGATTGAAATATATACATTTCTAT 1494
Qy 61 GATCAATCTCTTTTCTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAATGATTA 120
Db 1495 GATCAATCTCTTTTCTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAATGATTA 1554
Qy 121 GAAATGGAACCACTAGAGGAATATAATGTCTTAGGAAATTTACAGTCAATTTCTTAAGGGCC 180
Db 1555 GAAATGGAACCACTAGAGGAATATAATGTCTTAGGAAATTTACAGTCAATTTCTTAAGGGCC 1614
Qy 181 CAGCCCTTTGACAAAATTTGTGAAGTTTAAATTTCTCCACTCTGTCCTCATCAGATCTATGTTTC 240
Db 1615 CAGCCCTTTGACAAAATTTGTGAAGTTTAAATTTCTCCACTCTGTCCTCATCAGATCTATGTTTC 1674
Qy 241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTTAGCAGCAATTCATCTTCCCGAT 300
Db 1675 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTTAGCAGCAATTCATCTTCCCGAT 1734
Qy 301 CTTCTTTCTCTCTCCAAACCAACATCAATGTATTATAGTTCTGTATACAGTACAGGATC 360
Db 1735 CTTCTTTCTCTCTCCAAACCAACATCAATGTATTATAGTTCTGTATACAGTACAGGATC 1794
Qy 361 TTTGTCTACTCTATCACAGGCCAGTACCACTCATGAAGAAAGAACACAGAGTAGC 420
Db 1795 TTTGTCTACTCTATCACAGGCCAGTACCACTCATGAAGAAAGAACACAGAGTAGC 1854
Qy 421 TGAGAGGCTAAAACCTCATCAAAAACACTACTCTCTTTTCTCTACCCCTATTCCTCAATCTT 480
Db 1855 TGAGAGGCTAAAACCTCATCAAAAACACTACTCTCTTTTCTCTACCCCTATTCCTCAATCTT 1914
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCTCTCTCC 540
Db 1915 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCTCTCTCTCC 1974
Qy 541 TTTTACCCTCCATGTCGTTAAAGGAGAGATGGGGAGCATCATCTGTTATCTTCTGTA 600
Db 1975 TTTTACCCTCCATGTCGTTAAAGGAGAGATGGGGAGCATCATCTGTTATCTTCTGTA 2034
Qy 601 CACAGTTATACATGTCATCAAAACCAGACTTGTCTTCCATAGTGAGAGACTTGTCTTTTCCAG 660
Db 2035 CACAGTTATACATGTCATCAAAACCAGACTTGTCTTCCATAGTGAGAGACTTGTCTTTTCCAG 2094
Qy 661 AACATAGGAGTGAAGTGAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTT 720
Db 2095 AACATAGGAGTGAAGTGAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTT 2154
Qy 721 AAGTTATTTTAG 780
Db 2155 AAGTTATTTTAG 2214
Qy 781 TGTGTGTGTGTATGCGT 840
Db 2215 TGTGTGTGTGTATGCGT 2274

Qy	841	AGCCATTCCTAAGAGCTTGATGGTTATGAGAGGTCTGACTAGGCAAGATGATTTCAAGAGGCA	900
Db	2275	AGCCATTCCTAAGAGCTTGATGGTTATGAGAGGTCTGACTAGGCAAGATGATTTCAAGAGGCA	2334
Qy	901	AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	960
Db	2335	AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	2394
Qy	961	CTAAAAATAAATAAATAAATGCTTAACAGAAAGAGAGAACCGTTTCGTTTGCATCTACAG	1020
Db	2395	CTAAAAATAAATAAATAAATGCTTAACAGAAAGAGAGAACCGTTTCGTTTGCATCTACAG	2454
Qy	1021	CTAGTAGAGACTTTGAGGAAGATTTCAACAGTGTGCTTCAGCAGTGTTCAGAGCCCAAGC	1080
Db	2455	CTAGTAGAGACTTTGAGGAAGATTTCAACAGTGTGCTTCAGCAGTGTTCAGAGCCCAAGC	2514
Qy	1081	AAGAAGTTGAAGTTGCCTTAGACAGAGGAGATAGTATCATGTCTCCTTTAACTAGCAT	1140
Db	2515	AAGAAGTTGAAGTTGCCTTAGACAGAGGAGATAGTATCATGTCTCCTTTAACTAGCAT	2574
Qy	1141	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAAGGCATAAGTTCATTTCCATCAGCCAACT	1200
Db	2575	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAAGGCATAAGTTCATTTCCATCAGCCAACT	2634
Qy	1201	AAGTTGCTCTTTCTCGTTTCGTTTCACCATGGAACATTTGATATAGTTAATCCTTC	1260
Db	2635	AAGTTGCTCTTTCTCGTTTCGTTTCACCATGGAACATTTGATATAGTTAATCCTTC	2694
Qy	1261	TATCTTGAATCTT 1273	
Db	2695	TATCTTGAATCTT 2707	

RESULT 3

US-10-133-907-2

; Sequence 2, Application US/10133907

; Patent No. 6677369

; GENERAL INFORMATION:

; APPLICANT: Chien, Kenneth R

; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII

; TITLE OF INVENTION: with vesicle vector

; FILE REFERENCE: 6627-PALL170

; CURRENT APPLICATION NUMBER: US/10/133.907

; CURRENT FILING DATE: 2002-04-25

; PRIOR APPLICATION NUMBER: 60/286,314

; PRIOR FILING DATE: 2001-04-25

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 2804

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-133-907-2

Query Match 100.0%; Score 1273; DB 4; Length 2804;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTCTCACTAATACTATTTCCCATCTTTGTTAGATTTGAATATATACATTTCTAT 60

Db 1464 GGCCTCTCACTAATACTATTTCCCATCTTTGTTAGATTTGAATATATACATTTCTAT 1523

Qy 61 GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAATTCATTA 120

Db 1524 GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAATTCATTA 1583

Qy 121 GAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTCAGTCATTTCTAAGGGCC 180

Db 1584 GAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTCAGTCATTTCTAAGGGCC 1643

Qy 181 CAGCCCTTGACAAATTTGAAGTTAAATTTCTCCACTCTGTCATCAGATACATATGTTTC 240

Db	1644	CAGCCCTTGACAAAATTGTGAAGTTAAATTTCTCCACTCTGTGCCATCAGATACTATGGTTC	1703
Qy	241	TCCACTATGGCAACTAACTCACTCAAAATTTTCCCTCCCTTAGCAGCATTTCCATCTTCCCGAT	300
Db	1704	TCCACTATGGCAACTCACTCAAAATTTTCCCTCCCTTAGCAGCATTTCCATCTTCCCGAT	1763
Qy	301	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	360
Db	1764	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	1823
Qy	361	TTTGGTCTACTCTATCAACAAGGCCAGTACACACTCATGAAGAAGAACACAGAGATGAGC	420
Db	1824	TTTGGTCTACTCTATCAACAAGGCCAGTACACACTCATGAAGAAGAACACAGAGATGAGC	1883
Qy	421	TGAGAGGCTAAAACTCATCAAAAACACTACTCTCTTTTCCCTCTACCCCTATTCTCAATCTT	480
Db	1984	TGAGAGGCTAAAACTCATCAAAAACACTACTCTCTTTTCCCTCTACCCCTATTCTCAATCTT	1943
Qy	481	TTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTTCTTACTCCCTCTCTCCCC	540
Db	1944	TTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTTCTTACTCCCTCTCTCCCC	2003
Qy	541	TTTTTACCCTCCATGGTGGTTAAAGGAGAGATGGGAGCATCATCTGTATATCTTCTGTATA	600
Db	2004	TTTTTACCCTCCATGGTGGTTAAAGGAGAGATGGGAGCATCATCTGTATATCTTCTGTATA	2063
Qy	601	CACAGTTATACATGTCCTATCAAAACCCAGACTTGCCTCCATAGTGGAGACTTGTCTTTTCAG	660
Db	2064	CACAGTTATACATGTCCTATCAAAACCCAGACTTGCCTCCATAGTGGAGACTTGTCTTTTCAG	2123
Qy	661	AACATAGGGATGAAGTAAGTGGCTGAAAAAGTTTGGGGGAAAAAGTTTCTTTTCAGAGATTT	720
Db	2124	AACATAGGGATGAAGTAAGTGGCTGAAAAAGTTTGGGGGAAAAAGTTTCTTTTCAGAGATTT	2183
Qy	721	AAGTTATTTATATATATAATATATATAAAATATATAATATATAAATATAATATATATAG	780
Db	2184	AAGTTATTTATATATATAATATATATAAAATATATAATATAAATATAATATATATAG	2243
Qy	781	TGTTGTGTGTATGTCGTGTGTAGACACACAACGCATACACATATAATATGGAAGCAATA	840
Db	2244	TGTTGTGTGTATGTCGTGTGTAGACACACAACGCATACACATATAATATGGAAGCAATA	2303
Qy	841	AGCCATTTCAAGAGCTTGTTATGGTTATGGAGGTCTGACTAGGCATGATTTTCAGGAAGCA	900
Db	2304	AGCCATTTCAAGAGCTTGTTATGGTTATGGAGGTCTGACTAGGCATGATTTTCAGGAAGCA	2363
Qy	901	AGATTGGCATATCATTTGTAACTAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	960
Db	2364	AGATTGGCATATCATTTGTAACTAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTT	2423
Qy	961	CTAAAAATATAATAATAATGCTTAACAGAAGAAGAGAACCGTTTCGTTTGCATCTACAG	1020
Db	2424	CTAAAAATATAATAATAATGCTTAACAGAAGAAGAGAACCGTTTCGTTTGCATCTACAG	2483
Qy	1021	CTAGTAGAGACTTTGAGGAAGAAATTCAAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAAGC	1080
Db	2484	CTAGTAGAGACTTTGAGGAAGAAATTCAAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAAGC	2543
Qy	1081	AAGAAGTTGAAGTTGCTCTAGACAGAGGACATTAAGTATCAATGTCTCTTTTAACTAGCATTA	1140
Db	2544	AAGAAGTTGAAGTTGCTCTAGACAGGAGGACATTAAGTATCAATGTCTCTTTTAACTAGCATTA	2603
Qy	1141	CCCCGAAGTGGAGAGGGTGCACAGGCTCAAAAGGCATAGTCAATCCCAATCAGCCAACT	1200
Db	2604	CCCCGAAGTGGAGAGGGTGCACAGGCTCAAAAGGCATAGTCAATCCCAATCAGCCAACT	2663
Qy	1201	AAGTTGTCTCTTTTCTGGTTTCTGGTTTCCCATGGAACTTTTGAATATAGTTAATCCTTC	1260
Db	2664	AAGTTGTCTCTTTTCTGGTTTCTGGTTTCCCATGGAACTTTTGAATATAGTTAATCCTTC	2723
Qy	1261	TATCTTGAATCTTT	1273
Db	2724	TATCTTGAATCTTT	2736

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RESULT 4
US-09-328-925-4
; Sequence 4, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 38059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-925-4

Query Match 100.0%; Score 1273; DB 4; Length 38059;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCTCTCACTAACTCACTTCCCATCTTTGTTAGATTGTAATATATACATCTAT 60
DB 34383 GGCCTCTCACTAACTCACTTCCCATCTTTGTTAGATTGTAATATATACATCTAT 34442
QY 61 GATCATTTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATGATTA 120
DB 34443 GATCATTTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATGATTA 34502
QY 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGAAATACAGTCATTTCTAAGGGCC 180
DB 34503 GAAATGGAACCACTAGAGGAATATAATGTGTAGAAATACAGTCATTTCTAAGGGCC 34562
QY 181 CAGCCCTTGACAAATTTGGAAGTTAAATTTCCACTCTGTCATCAGTACTATGGTTC 240
DB 34563 CAGCCCTTGACAAATTTGGAAGTTAAATTTCCACTCTGTCATCAGTACTATGGTTC 34622
QY 241 TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTACGAGCAATTCCTCCGAT 300
DB 34623 TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTACGAGCAATTCCTCCGAT 34682
QY 301 CTTCTTTGCTTCTCCAAACCAATCAATCAATGTTTATAGTTCTGTATACAGTACAGGATC 360
DB 34683 CTTCTTTGCTTCTCCAAACCAATCAATCAATGTTTATAGTTCTGTATACAGTACAGGATC 34742
QY 361 TTTGCTTACTCTATCAGAGCCAGTACCACTCATGAAAGAAACACAGGAGTAGC 420
DB 34743 TTTGCTTACTCTATCAGAGCCAGTACCACTCATGAAAGAAACACAGGAGTAGC 34802
QY 421 TGAGAGGCTTAAACTCATCAAAACCACTACTCTTTCTCTACCTATTTCTCTCAATCTT 480
DB 34803 TGAGAGGCTTAAACTCATCAAAACCACTACTCTTTCTCTACCTATTTCTCTCAATCTT 34862
QY 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTCTTTACTCCCTCTCTCC 540
DB 34863 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTCTTTACTCCCTCTCTCC 34922
QY 541 TTTTACCTCCCTCAATGCTGTTAAAGGAGAGATGGGAGCATCTCTGTTATATCTCTGA 600
DB 34923 TTTTACCTCCCTCAATGCTGTTAAAGGAGAGATGGGAGCATCTCTGTTATATCTCTGA 34982
QY 601 CACAGTTATACATGCTATCAAAACCCAGACTTGTCTTCCATAGTGAGACTTCTGTTTTCAG 660
DB 34983 CACAGTTATACATGCTATCAAAACCCAGACTTGTCTTCCATAGTGAGACTTCTGTTTTCAG 35042
QY 661 AACATAGGATGAAGTAAAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTTCAGAGAGTT 720
DB 35043 AACATAGGATGAAGTAAAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTTCAGAGAGTT 35102

RESULT 5
US-09-328-925-83
; Sequence 83, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-328-925-83

Query Match 99.9%; Score 1272; DB 4; Length 1272;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCTCTCACTAACTCAATCACTTCCCATCTTTGTTAGATTGTAATATATACATCTATG 61
DB 1 GCCTCTCACTAACTCAATCACTTCCCATCTTTGTTAGATTGTAATATATACATCTATG 60
QY 62 ATCATTTGCTTTTCTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTG 121
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16994
; LENGTH: 36755
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16994

Query Match          99.9%; Score 1271.4; DB 4; Length 36755;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GGCCTCTCACTAACTCACTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT 60
DB      33414  GGCCTCTCACTAACTCACTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT 33473

QY      61  GATCATTTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA 120
DB      33474  GATCATTTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA 33533

QY      121  GAAATGGAAACCACTAGAGGAATATATGTTAGGAATTAACAGTCATTTCTAAGGGCC 180
DB      33534  GAAATGGAAACCACTAGAGGAATATATGTTAGGAATTAACAGTCATTTCTAAGGGCC 33593

QY      181  CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACCTATGTTTC 240
DB      33594  CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACCTATGTTTC 33653

QY      241  TCACATATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCATTCCTCCGAT 300
DB      33654  TCACATATGGCACTAACTCACTCAATTTTCCCTCTTAGCAGCATTCCTCCGAT 33713

QY      301  CTTCTTTGCTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
DB      33714  CTTCTTTGCTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 33773

QY      361  TTTGGTCTACTCTATCACAAGGCCAGTACCACTCATGAAGAAAGAACACAGGAGTAGC 420
DB      33774  TTTGGTCTACTCTATCACAAGGCCAGTACCACTCATGAAGAAAGAACACAGGAGTAGC 33833

QY      421  TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTCTCTACCCCTATTCCTCAATCTT 480
DB      33834  TGAGAGGCTAAACTCATCAAAAACACTACTCTCTCTCTACCCCTATTCCTCAATCTT 33893

QY      481  TTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTCTTACTCCCTCTCTCC 540
DB      33894  TTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTCTTACTCCCTCTCTCC 33953

QY      541  TTTTACCCCTCCATGGTCGTTAAAGAGAGAGATGGGAGCATCAATCTGTTATATCTCTGTA 600
DB      33954  TTTTACCCCTCCATGGTCGTTAAAGAGAGATGGGAGCATCAATCTGTTATATCTCTGTA 34013

QY      601  CACAGTTATACATGCTTATCAAAACCAGACTTGTCTTCCATAGTGGAGACTGCTTTTCAG 660
DB      34014  CACAGTTATACATGCTTATCAAAACCAGACTTGTCTTCCGATGAGAGACTGCTTTTCAG 34073

QY      661  AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
DB      34074  AACATAGGATGAAGTAAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 34133

QY      721  AAGTTATTTTATATATATATATATATAATAATATATATAATAATAATAATATATATAG 780
DB      34134  AAGTTATTTTATATATATATATATATAATAATAATAATAATAATAATAATATATATAG 34193

QY      781  TGTGTGTGTATGCGTGTGTGTAGACACACACGATACACATATATATATATATATATATAT 840
DB      34194  TGTGTGTGTGTATGCGTGTGTGTAGACACACACGATACACATATATATATATATATATAT 34253

QY      841  AGCCCAATTTCTAAGAGCTGCTGATGGTTTATGAGTCTGACTAGGCATGATTTTACGAAGGCA 900
DB      34254  AGCCCAATTTCTAAGAGCTGCTGATGGTTTATGAGTCTGACTAGGCATGATTTTACGAAGGCA 34313

QY      901  AGATTGGCATATCATTTGTAACCTAAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTT 960
DB      34314  AGATTGGCATATCATTTGTAACCTAAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTT 34373

QY      961  CTAAAAATAATAATAATAATAATGCTAAACAGAAAGAGAACCGTTTGGTTTGCATCTACAG 1020
DB      34374  CTAAAAATAATAATAATAATAATGCTAAACAGAAAGAGAACCGTTTGGTTTGCATCTACAG 34433

QY      1021  CTAGTAGAGACTTTTGAGGAAGAAATTTCAACAGTGTGCTTTCAGCAGTGTTCAGAGCCAAAGC 1080
DB      34434  CTAGTAGAGACTTTTGAGGAAGAAATTTCAACAGTGTGCTTTCAGCAGTGTTCAGAGCCAAAGC 34493

QY      1081  AAGAAAGTTGAAGTTCCCTAGACGAGACATAAGTATCATGTCTCTCTTTAACTAGCATATA 1140
DB      34494  AAGAAAGTTGAAGTTCCCTAGACGAGACATAAGTATCATGTCTCTCTTTAACTAGCATATA 34553

QY      1141  CCCCAGAGTGAGAAAGGTGACAGAGGCTCAAAAGGCATAAGTCATTCCAATCAGCCAACT 1200
DB      34554  CCCCAGAGTGAGAAAGGTGACAGAGGCTCAAAAGGCATAAGTCATTCCAATCAGCCAACT 34613

QY      1201  AAGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGAATATAGTTAACTCTTC 1260
DB      34614  AAGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGAATATAGTTAACTCTTC 34673

QY      1261  TATCTTGAATCTT 1273
DB      34674  TATCTTGAATCTT 34686
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RESULT 10

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US-09-328-925-78
; Sequence 78, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-328-925-78
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Query Match          99.7%; Score 1269.8; DB 4; Length 1273;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GGCCTCTCACTAACTCACTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT 60
DB      1  GGCCTCTCACTAACTCACTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT 60

QY      61  GATCATTTGCTTTTCTTTTACAGGGGAGAAATTTCAATATTTTACCTGAGCAAAATTGATTA 120
DB      61  GATCATTTGCTTTTCTTTTACAGGGGAGAAATTTCAATATTTTACCTGAGCAAAATTGATTA 120
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121 GAAATGGAACCACTAGAGGAATATATATGTTGTAGGAAATTA CAGTCATTTCTAAGGGCC 180
121 GAAATGGAACCACTAGAGGAATATATATGTTGTAGGAAATTA CAGTCATTTCTAAGGGCC 180
181 CAGCCCTTGACAAATTTGCAAGTTAAATTTCTCCACTCTGCTCCATCAGATACATATGGTTC 240
181 CAGCCCTTGACAAATTTGCAAGTTAAATTTCTCCACTCTGCTCCATCAGATACATATGGTTC 240
241 TCCACTATGCAACTAACTCACTCAATTTTCCCTCTCTTAGCAGCATTTCCATCTTCCCGAT 300
241 TCCACTATGCAACTAACTCACTCAATTTTCCCTCTCTTAGCAGCATTTCCATCTTCCCGAT 300
301 CTTCTTGTCTTCCCAACCAAAACATCAATGTTTATAGTTCTGTATACAGTACAGATC 360
301 CTTCTTGTCTTCCCAACCAAAACATCAATGTTTATAGTTCTGTATACAGTACAGATC 360
361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTACC 420
361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTACC 420
421 TGAGAGGCTAAACTCATCAAAACCACTACTCTCTTCTCTACCTCTATTCCTCAATCTT 480
421 TGAGAGGCTAAACTCATCAAAACCACTACTCTCTTCTCTACCTCTATTCCTCAATCTT 480
481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 540
481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCA 540
541 TTTTACCTCCCTGCTGTTTAAAGGAGAGATGGGAGCATCTCTGTTATATCTTCTGTA 600
541 TTTTACCTCCCTGCTGTTTAAAGGAGAGATGGGAGCATCTCTGTTATATCTTCTGTA 600
601 CACAGTTATACATGCTCTATCAAAACCCAGACTCTCTTCCATAGTGGAGACTTGTCTTTCAG 660
601 CACAGTTATACATGCTCTATCAAAACCCAGACTCTCTTCCATAGTGGAGACTTGTCTTTCAG 660
661 AACATAGGATGAAGTAAAGTGGCTGAAAGTTTGGGGGAAAGTTTCTTTCAGAGATT 720
661 AACATAGGATGAAGTAAAGTGGCTGAAAGTTTGGGGGAAAGTTTCTTTCAGAGATT 720
721 AAGTTATTTAG 780
721 AAGTTATTTAG 780
781 TGTGTGTGTATGCTGTGTGTAGACACACACGATACACATATATATATATATATATATATATAG 840
781 TGTGTGTGTATGCTGTGTGTAGACACACACGATACACATATATATATATATATATATATAG 840
841 AGCCATTTCAAGAGCTTGTATGTTTATGAGGCTCTGACTAGGCATGATTTTCAGAGGCA 900
841 AGCCATTTCAAGAGCTTGTATGTTTATGAGGCTCTGACTAGGCATGATTTTCAGAGGCA 900
901 AGATTGGCATATCATTTGTAACCTTAAAGGCTGACATTTGACCCAGACATATTTGACTCTTT 960
901 AGATTGGCATATCATTTGTAACCTTAAAGGCTGACATTTGACCCAGACATATTTGACTCTTT 960
961 CTAATA 1020
961 CTAATA 1020
1021 CTAGTAGAGACTTTGAGGAAGATTTCAACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAAGC 1080
1021 CTAGTAGAGACTTTGAGGAAGATTTCAACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAAGC 1080
1081 AAGAAGTTCAAGTTGCTTACAGAGGACATTAAGTATCATGTCTCTCTTAACTAGCATA 1140
1081 AAGAAGTTCAAGTTGCTTACAGAGGACATTAAGTATCATGTCTCTCTTAACTAGCATA 1140
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1201 AAGTTGTCTCTTCTGTTTCTGTTTCCACCATGGAACATTTTGAATATAGTAAATCTCTCC 1260

RESULT 11

US-09-118-748-1
; Sequence 1, Application US/09118748A
; Patent No. 6531298
; GENERAL INFORMATION:
; APPLICANT: Stafford, Darrel W.
; APPLICANT: Chang, JinLi
; TITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting
; FILE REFERENCE: 5470-183
; CURRENT APPLICATION NUMBER: US/09/118,748A
; EARLIER FILING DATE: 1998-07-17
; EARLIER FILING DATE: 1997-07-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2792
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence of
; OTHER INFORMATION: human factor IX-R338A
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (156)..(1400)
US-09-118-748-1

Query Match 99.7%; Score 1269.8; DB 4; Length 2792;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCCTCTCACTAACTAACTCACTTTCCCATCTTTGTTAGATTGTAATATATACATTTCTAT 60
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QY 61 GATCATTGCTTTTCTCTTTACAGGGGAGAAATTTACATTTTACCTGACCAATTCATTA 120
DB 1512 GATCATTGCTTTTCTCTTTACAGGGGAGAAATTTACATTTTACCTGACCAATTCATTA 1571
QY 121 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTAACAGTCATTTCTAAGGGCC 180
DB 1572 GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTAACAGTCATTTCTAAGGGCC 1631
QY 181 CAGCCCTTGACAAATTTGGAAGTTAAATTTCCACTCTGTCCATCAGATACATATGGTTC 240
DB 1632 CAGCCCTTGACAAATTTGGAAGTTAAATTTCCACTCTGTCCATCAGATACATATGGTTC 1691
QY 241 TCCACTATGGCACTTAACCTCACTCAATTTTCCCTCTTAGCAGCATTTCCATCTTCCCGAT 300
DB 1692 TCCACTATGGCACTTAACCTCACTCAATTTTCCCTCTTAGCAGCATTTCCATCTTCCCGAT 1751
QY 301 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATAGTTCTGTATACAGTACAGGATC 360
DB 1752 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATAGTTCTGTATACAGTACAGGATC 1811
QY 361 TTTGCTTACTCTATCAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420
DB 1812 TTTGCTTACTCTATCAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 1871
QY 421 TGAGAGGCTTAAACTCATCAAAACCACTACTCTCTTCTCTACCTATTCCTCAATCTT 480
DB 1872 TGAGAGGCTTAAACTCATCAAAACCACTACTCTCTTCTCTACCTATTCCTCAATCTT 1931
QY 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCTCTCTCC 540

; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; FILE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-328-925-80

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Best Local Similarity		99.8%;	Pred. No. 0;		
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				Indels	2;
				Gaps	1;
QY	1	GGCCTCTCACTAACTCACTTCCCATCTTTTGGTAGATTGAAATATATACATCTAT	60		
DB	1	GGCCTCTCACTAACTCACTTCCCATCTTTTGGTAGATTGAAATATATACATCTAT	60		
QY	61	GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTCATATTTACCTGAGCAAAATTCATTA	120		
DB	61	GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTCATATTTACCTGAGCAAAATTCATTA	120		
QY	121	GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTAAGTCATTTCTTAAGGGCC	180		
DB	121	GAAATGGAACCACTAGAGGAATATAATGTGTAGGAAATTAAGTCATTTCTTAAGGGCC	180		
QY	181	CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACATATGGTTC	240		
DB	181	CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACATATGGTTC	240		
QY	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTTCTTAGCAGCATTCCTCCGA-	299		
DB	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTTCTTAGCAGCATTCCTCCGAT	300		
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DB	301	TTCTTCTTTTCTTCTTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGA	360		
QY	359	TCTTTGGTCTACTCTATCAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGATTA	418		
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QY	419	GCTGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTTCTTACCCTATTCCTCAATC	478		
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QY	479	TTTTTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTTCTTACTCCCTCTCTC	538		
DB	481	TTTTTACCTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTTCTTACTCCCTCTCTC	540		
QY	539	CTTTTACCTCTCATCGTGTAAAGGAGAGATGGGGAGCATCTCTGTATATCTTCG	598		
DB	541	CTTTTACCTCTCATCGTGTAAAGGAGAGATGGGGAGCATCTCTGTATATCTTCG	600		
QY	599	TACACAGTTATACATGCTCATCAAAACCCAGCTTGCTTCCATAGTGGAGACTTGTCTTTC	658		
DB	601	TACACAGTTATACATGCTCATCAAAACCCAGCTTGCTTCCATAGTGGAGACTTGTCTTTC	660		
QY	659	AGAACATAGGATGAAGTAAAGTCTGAAAGTTTGGGGAAAGTTTCTTTCAGAGAG	718		
DB	661	AGAACATAGGATGAAGTAAAGTCTGAAAGTTTGGGGAAAGTTTCTTTCAGAGAG	720		
QY	719	TTAAGTTATTTATATATATATATATATAATAATAATAATAATAATAATAATAATAATA	778		
DB	721	TTAAGTTATTTATATATATATATATATAATAATAATAATAATAATAATAATAATAATA	780		
QY	779	AGTGTGTGTGTGTCGTTGTAGACACACACGACATACACATATAATGGAAGCAA	838		

Search completed: October 4, 2005, 13:36:33
Job time : 212 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 14:53:20 ; Search time 3943 Seconds
(without alignments)
12289.073 Million cell updates/sec

Title: US-10-018-392A-3
Perfect score: 1273
Sequence: 1 ggcctctcctaactaataca.....atcctctatattgaatttt 1273

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	776.4	61.0	943	5	BX405727
2	527.2	41.4	532	6	CB156936
C 3	456	35.8	515	5	BX414387
4	373	29.3	373	1	AV647038
5	373	29.3	374	1	AV647182
6	299.2	23.5	524	7	CO775183
7	273	21.4	385	1	AV656454
8	203	15.9	518	8	AQ456663
9	149.6	11.8	374	7	CF106639
10	149.6	11.8	688	5	BX926315
11	149.6	11.8	690	5	BX925779
12	147	11.5	257	7	CO775581
13	120.6	9.5	583	7	CO740602
C 14	107.4	8.4	592	9	CE730574
15	95.8	7.5	816	6	CA456053
16	86.6	6.8	525	5	BX514685
17	76	6.0	539	1	AA209011
18	73	5.7	507	1	AA270287
C 19	72.6	5.7	464	5	BP101424
C 20	68.8	5.4	389	5	BP102450
C 21	66.2	5.2	400	7	CO701325
C 22	66.2	5.2	583	5	BP103684
C 23	63.4	5.0	841	8	AQ782305
C 24	62.8	4.9	574	5	BP104057

C 25	62.2	4.9	1101	9	CNS0039G	AL063921 Drosophila
C 26	60.8	4.8	1029	9	CNS0017V	AL074642 Drosophila
C 27	60.8	4.8	1101	9	CNS0039G	AL063921 Drosophila
C 28	60.2	4.7	468	8	AZ904168	AZ904168 RPCI-24-1
C 29	58.8	4.6	623	6	CD473714	CD473714 nad03-10m
C 30	57.2	4.5	532	8	BH180068	BH180068 016 M 07-
C 31	57.2	4.5	532	9	CNS07MOC	AL617022 T3_end of
C 32	56	4.4	736	9	AG462569	AG462569 Mus muscu
C 33	55.6	4.4	430	2	AW631271	AW631271 hh80d01.y
C 34	54.8	4.3	557	1	AI425351	AI425351 mx89e10.y
C 35	54.8	4.3	684	9	AG091777	AG091777 Pan trogl
C 36	54.6	4.3	469	8	AZ387095	AZ387095 1M0146G20
C 37	54.6	4.3	735	7	CO567891	CO567891 AGENCOURT
C 38	54.4	4.3	522	8	AQ483469	AQ483469 RPCI-11-2
C 39	54.4	4.3	571	7	CNI95227	CNI95227 T9ESTy18
C 40	54.2	4.3	722	8	AZ987360	AZ987360 2M0269H23
C 41	54.2	4.3	1101	9	CNS0100X	AL098379 Drosophila
C 42	53.8	4.2	424	8	AQ023352	AQ023352 HS-2179 B
C 43	53.8	4.2	902	9	CNS000CVM	AL060007 Drosophila
C 44	53.6	4.2	753	9	AG294270	AG294270 Mus muscu
C 45	53.4	4.2	680	7	CO567171	CO567171 AGENCOURT

ALIGNMENTS

RESULT 1
BX405727/c
LOCUS BX405727 Homo sapiens FETAL LIVER Homo sapiens CDNA clone
DEFINITION CSODM008Y108 3-PRIME, mRNA sequence.
ACCESSION BX405727
VERSION BX405727
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 943)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30635411.
Contact: Genoscope
Genoscope - Centre National de Séquencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 10715.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSOAM008B04NP16c=10715.f.
Location/Qualifiers
1. .943
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODM008Y108"
/tissue type="FETAL LIVER"
/dev stage="fetal"
/clone lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match 61.0%; Score 776.4; DB 5; Length 943;
Best Local Similarity 89.7%; Pred. No. 4.4e-170;

Matches	819;	Conservative	47;	Mismatches	39;	Indels	8;	Gaps	4;
Qy	362	TTGCTCTACTCTATCAAGGCCAGTACCACTCATGAAGAAAGAAACACAGGAGTAGCT	421						
Db	943	TTGGTCCAAAAATCAACAGCCAGKWCYARACTCATSTRGAGAGATCACGSGKAGCT	884						
Qy	422	GAGAGGCTAAACTCATCAAAAAACACTACTCTCTTTTCTCTACCCATTTCTCTCAATCTTT	481						
Db	883	GMGYKSCTAAATTTCTTY-AAAAAMTACTCC-TTTACTCTTMMCTATTACAMAATCTTT	826						
Qy	482	TACCTTTTCCAAATCCCAATCCCC-AAATCAGTTTTTCTCTTCTTACTCCCTCTCTCCC	540						
Db	825	NACCATTTCAAAATCMWAATCCCCMAAATCAGTTTTTCTCTTCTTACTCCCTATCTCCC	766						
Qy	541	TTTTACCCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTTCTGTATCTTCTGTA	600						
Db	765	TTTTACCCCTCCATSRCTRTTTAAAGGAGAGATGGGKMGCATCWTCTATCTTMTGAA	706						
Qy	601	CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTTCAG	660						
Db	705	CACAGWTATACATGCTCTATMAAACCCAACTCKTWMCTTTADTGGAAAHTTGCTCTTMMAG	646						
Qy	661	AACATAGGATGAAGTAGAGTGCTGAAAGCTTTGGGGGAAAGTTCTTTTCAGAGAGTT	720						
Db	645	AACATAGGATGAAGTAGAGTGCTGWAAGTTTGGGGGAAAGTCTCTCTCASASAST	586						
Qy	721	AAGTTATTTTATATATATATATATATAATAATAATAATAATAATAATAATAATAATA	780						
Db	585	AAGTTATTTTWTATATATATATATATAATAATAATAATAATAATAATAATAATAATA	527						
Qy	781	TGTGTGTGTATCGGTGTGTGTATATAGGAGTCTGACTAGGCATGATTTTCACGAAGCAATA	840						
Db	526	----NGNTKGTGTTATGTGTGTGTAAACACACACGCATACACATATAATGGGAACATA	471						
Qy	841	AGCCATCTTAAGAGCTTGTATGTTTATGGAGTCTGACTAGGCATGATTTTCACGAAGCA	900						
Db	470	AGCCATCTTAAGAGCTTGTATGTTTATGGAGTCTGACTAGGCATGATTTTCACGAAGCA	411						
Qy	901	AGATTGGCATATCATGTGTAATAAAAGCTGACATTTGACCCAGACATATTTGTACTCTTT	960						
Db	410	AGATTGGCATATCATGTGTAATAAAAGCTTACATTTGACCCACATATTTGTACTCTTT	351						
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Qy	1021	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTGTTCTCAGCAGTGTTCAGAGCCCAAGC	1080						
Db	290	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTGTTCTCAGCAGTGTTCAGAGCCCAAGC	231						
Qy	1081	AAGAAGTTGAAGTTGCCTAGACACAGAGGACATAAGTATCATGTCTCTTTAACTAGCATATA	1140						
Db	230	AAGAAGTTGAAGTTGCCTAGACACAGAGTACATAAGTATCATGTCTCTTTAACTAGCATATA	171						
Qy	1141	CCCCGAAGTGGAGAAGGTGCAGCAGGCTCAAGGCATAGTCAATTCCAATCAGCCCACT	1200						
Db	170	CCCCGAAGTGGAGAAGGTGCAGCAGGCTCAAGGCATAGTCAATTCCAATCAGCCCACT	111						
Qy	1201	AAGTTGTCTTTTCTGGTTTCGTGTTTCCACTGGAACATTTTGATTTATAGTTAATCTTTC	1260						
Db	110	AAGTTGTCTTTTCTGGTTTCGTGTTTCCACTGGAACATTTTGATTTATAGTTAATCTTTC	51						
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Db	50	TATCTTGAATCTT 38							

RESULT 2	CB156936	532 bp	linear	EST 29-JAN-2003
LOCUS	CB156936			
DEFINITION	K-EST0215940	L17N670205n1	Homo sapiens	cdna clone
		L17N670205n1-6-A08	5',	mRNA sequence.
ACCESSION	CB156936			

VERSION	CB156936.1										GI:28142066
KEYWORDS	EST.										
SOURCE	Homo sapiens (human)										
ORGANISM	Homo sapiens										
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.										
AUTHORS	1 (bases 1 to 532) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.										
TITLE	21C Frontier Korean EST Project 2001										
JOURNAL	Unpublished (2002)										
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 6 row: A column: 08 High quality sequence stop: 532.										
FEATURES	Location/Qualifiers										
source	1..532 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="L17N670205n1-6-A08" /sex="F" /lab_host="Top10P" /clone_lib="L17N670205n1" /note="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."										
ORIGIN											
Query Match	41.4%; Score 527.2; DB 6; Length 532;										
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Matches 529;	Conservative 0; Mismatches 3; Indels 0; Gaps 0;										
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Qy	155 GGAAATTAAGTCAATTTCTAAGGCCCCAGGCCCTTGACAAAATGTGAAGTTAAATTCCTC 214										
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Qy	215 ACTCTGTCCATCAGATACTAGTGTCTCCCACTATGGCACTAACTCACTCAATTTCCCT 274										
Db	121 ACTCTGTCCATCAGATACTAGTGTCTCCCACTATGGCACTAACTCACTCAATTTCCCT 180										
Qy	275 CCTTAGCAGCAATCCATCTTCCCCGATCTTCTTTCCTTCTCCAAACCAAAACATCAATGTTT 334										
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Qy	335 ATTAGTTCCTGATACAGTACAGGATCTTTGGTCTACTCTATCACAAGGCCAGTACCACAC 394										
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Qy	395 TCATGAAGAAGACACAGGATAGCTGAGAGGCTTAAACTCATCAAAACACTACTCTCT 454										
Db	301 TCATGAAGAAGACACAGGATAGCTGAGAGGCTTAAACTCATCAAAACACTACTCTCT 360										
Qy	455 TTTCTCTACCTATTCTCTCAATCTTTTACCTTTTCCAAATCCCAATCCCAATTCAGTT 514										
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Qy	515 TTTCTCTTTCTACTCCCTCTCTCCCTTTTACCTCTCATGGTGTAAAGGAGATGGG 574										
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Qy 575 GAGCATCATCTTCTGTATACCTTCTGTACACAGTTATACATGCTCTATCAAAACC 626
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Db 481 GAGCATCATCTTCTGTATACCTTCTGTACACAGTTATACATGCTCTATCAAAACC 532
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RESULT 3
BX414387/c
LOCUS BX414387 Homo sapiens FETAL LIVER Homo sapiens cDNA clone linear EST 01-MAY-2004
DEFINITION CS0DM008Y108 3-PRIME, mRNA sequence.
ACCESSION BX414387
VERSION BX414387.2 GI:46928493
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
AUTHORS Full-length cDNA libraries and normalization
TITLE Unpublished (2001)
JOURNAL On May 13, 2003 this sequence version replaced gi:30645720.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 10715.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CS08AK078AH02NM1&c=10715.f.

FEATURES
source
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/db_xref="taxon:9606"
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Query Match 35.8%; Score 456; DB 5; Length 515;
Best Local Similarity 99.8%; Pred. No. 1.9e-95;
Matches 456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 515 TNCACACATATATGAAGCAATTAAGCCATTTCTAAGAGCTTGTATGTTATGAGGCTCTG 456
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Qy 877 ACTAGGCATGATTTTCAGGAAGCAAGATTGGGCATATCATTTGTAACATAAAAGCTGCAT 936
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Db 455 ACTAGGCATGATTTTCAGGAAGCAAGATTGGGCATATCATTTGTAACATAAAAGCTGCAT 396
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Qy 937 TGACCCAGACATATTTCTACTCTTTCTTCTAAAATAATAATAATATGCTAACAGAAAGA 996
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Db 395 TGACCCAGACATATTTCTACTCTTTCTTCTAAAATAATAATAATATGCTAACAGAAAGA 336
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Qy 997 GAACCCGTTTCGTTTGCATCTTACAGCTAGTAGACATTTTGAGGAAGAAATTCACAGTGTGT 1056
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Db 335 GAACCCGTTTCGTTTGCATCTTACAGCTAGTAGACATTTTGAGGAAGAAATTCACAGTGTGT 276
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Qy 1057 CTTACAGAGTTTCAGAGCCAAAGAAAGTTGAAGTTGCCTTAGCAGGAGCATATAAGT 1116
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Db 275 CTTACAGAGTTTCAGAGCCAAAGAAAGTTTGAAGTTGCCTTAGCAGGAGCATATAAGT 216
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Qy 1117 ATCATGTCCTCTTTAACTAGCATACCCGGAAGTGGAGAGGGTGCAGCAGGCTCAAAGGC 1176
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Qy 1177 ATAAGTCATTCCTCAATCAGCAACTAAGTTGTCTCTTTTCGTGGTTTCGTGTTCCACATGGAA 1236
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Db 155 ATAAGTCATTCCTCAATCAGCAACTAAGTTGTCTCTTTTCGTGGTTTCGTGTTCCACATGGAA 96
|||||
Qy 1237 CATTTTGTATATAGTTAAATCTCTTCTATCTTGAATCTT 1273
|||||
Db 95 CATTTTGTATATAGTTAAATCTCTTCTATCTTGAATCTT 59
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RESULT 4
AV647038
LOCUS AV647038 GLC Homo sapiens cDNA clone GLCAUA09 3', mRNA linear EST 15-JAN-2002
DEFINITION AV647038
ACCESSION AV647038
VERSION AV647038.1 GI:9868052
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
AUTHORS Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Lu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z. and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
11752456
COMMENT Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. 373
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCAUA09"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GLC"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 29.3%; Score 373; DB 1; Length 373;
Best Local Similarity 100.0%; Pred. No. 4.1e-76;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 GCTTTTCTCTTTACAGGGGAGATTTTCATATTTTACCTGAGCAATTCATTAGAAAATG 127
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Db 1 GCTTTTCTCTTTACAGGGGAGATTTTCATATTTTACCTGAGCAATTCATTAGAAAATG 60
|||||

Qy 128 GAACCACTAGAGGAATATATGTTAGGAAATTCACAGTCATTTCCTAACGGCCGCCCT 187
|||||
Db 61 GAACCACTAGAGGAATATATGTTAGGAAATTCACAGTCATTTCCTAACGGCCGCCCT 120
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Qy 188 TGACAAAATTTGAAAGTTAAATTTCCCACTCTGTCCATCAGATATCTATGTTCTCCACTA 247
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Db 121 TGACAAAATTGTGAAGTTAAATTTCTCGACTCTCTGTCATCAGATACATCTATGGTTCTCCACTA 180

Qy 248 TGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCATCTTCCGATCTTCTTT 307

Db 181 TGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCATCTTCCGATCTTCTTT 240

Qy 308 GCTTCTTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGATCTTTGGTC 367

Db 241 GCTTCTTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGATCTTTGGTC 300

Qy 368 TACTCTATCACAGGCCAGTACACACTCATGAAGAAAGAACACAGAGTAGCTGAGAG 427

Db 301 TACTCTATCACAGGCCAGTACACACTCATGAAGAAAGAACACAGAGTAGCTGAGAG 360

Qy 428 CTAAAACTCATCA 440

Db 361 CTAAAACTCATCA 373

RESULT 5
AV647182
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AV647182 374 bp mRNA linear EST 15-JAN-2002
AV647182 GLC Homo sapiens cDNA clone GLCAVF01 3', mRNA sequence.
AV647182.1 GI:9868196

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
XU, X., HUANG, J., XU, Z., QIAN, B., ZHU, Z., YAN, Q., CAI, T., ZHANG, X.,
XIAO, H., QU, J., LIU, F., HUANG, Q., CHENG, Z., LI, N., DU, J., HU, W.,
SHEN, K., LU, G., FU, G., ZHONG, M., XU, S., GU, W., HUANG, W., ZHAO, X.,
HU, G., GU, J., CHEN, Z. and HAN, Z.

TITLE
Insight into hepatocellular carcinogenesis at transcriptome level
with comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver

JOURNAL
MEDLINE
PUBMED
COMMENT
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

Location/Qualifiers
1..374
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCAVF01"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GLC"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

FEATURES
Source

ORGIN

Query Match 29.3%; Score 373; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.1e-76;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 GCTTTTCTCTTACAGGGGAGATTTCATATTATTTTACCTGAGCAATTCATTAGAAAATG 127

Db 1 GCTTTTCTCTTACAGGGGAGATTTCATATTATTTTACCTGAGCAATTCATTAGAAAATG 60

Qy 128 GAACCACTAGAGGAATATAATGTTAGGAATTCAGTCAATTTCTAAGGGCCCGCCCT 187

Db 61 GAACCACTAGAGGAATATAATGTTAGGAATTCAGTCAATTTCTAAGGGCCCGCCCT 120

Qy 188 TGACAAAATTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACATCTATGGTTCTCCACTA 247

Db 121 TGACAAAATTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACATCTATGGTTCTCCACTA 180

Qy 248 TGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCATCTTCCGATCTTCTTT 307

Db 181 TGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCATCTTCCGATCTTCTTT 240

Qy 308 GCTTCTTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGATCTTTGGTC 367

Db 241 GCTTCTTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGATCTTTGGTC 300

Qy 368 TACTCTATCACAGGCCAGTACACACTCATGAAGAAAGAACACAGAGTAGCTGAGAG 427

Db 301 TACTCTATCACAGGCCAGTACACACTCATGAAGAAAGAACACAGAGTAGCTGAGAG 360

Qy 428 CTAAAACTCATCA 440

Db 361 CTAAAACTCATCA 373

RESULT 6
C0775183
LOCUS
DEFINITION

C0775183 524 bp mRNA linear EST 04-AUG-2004
ILLUMIGEN MQO_52421 Katze MNUV Macaca nemestrina cDNA clone
IBIUM:28458 5' similar to Bases 5 to 424 highly similar to human F9
(Hs.1330), mRNA sequence.
C0775183
C0775183.1 GI:50976446

EST.
Macaca nemestrina (pig-tailed macaque)
Macaca nemestrina
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.07.21. 661 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org

PCR Primers
FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGCGGAATTCGGTA
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Place: CL000532 row: F column: 07
Seq primer: CCCTCACTAAAGGGAACAAAA
POLYA=Yes.

Location/Qualifiers
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/strain="Indian"
/db_xref="taxon:9545"
/clone="IBIUM:28458"
/sex="male"
/lab_host="Electromax DH108"
/clone_lib="Katze MNUV"
/note="Organ: Liver; Vector: pDONR 222; Site 1: BsrG I;
Site 2: BsrG I; Created from CloneMiner cDNA Library
Construction kit (catalog #18249-029)"

FEATURES
Source

ORGIN

Query Match 23.5%; Score 299.2; DB 7; Length 524;
Best Local Similarity 94.3%; Pred. No. 6.7e-59;
Matches 33; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 924 AAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTCTAAAAA-TAATAATAATATGC 982
DB 5 AAAAGCTGACATTTGACCGAGATATATTTGACTCTTTCTAAAAA-TAATAATAATATGC 64

QY 983 TAAACAGAAAGAGAACCGTTCTGTTGCAATCTACAGCTAGTAGAGACTTTTGGAGGA 1042
DB 65 TAAACAGAAAGAGAACAGCTCATTTGCGAGTCTACAACCTAGTAGAGACTTTTGGAGGA 124

QY 1043 ATTCAACAGTGTCTTTCAGCAGTGTTCAGAGCAAGCAAGAGTTGAAGTTCCCTAGAC 1102
DB 125 ATTCAACAGGCTGTCTTTCAGCAGTGTTCAGAGTCAAGAAAGAGTTGAAGTTCCCTAGAC 184

QY 1103 CAGAGGACATAAGTATCATGCTCTCTTTAACTAGCATACCCG-GAAGTGAGAGAGGTGC 1161
DB 185 CAGAGGACATAAGTATCATGCTCTCTTTAACTAGCATACCCGTTGAAGTTGAGAGAGGTGC 244

QY 1162 AGCAGGCTCAAGGACATAAGTATCAATCAATCAGCCCAACTAAGTTGTCCTTTTCTGGTTTC 1221
DB 245 AGCAGGCTCAAGGACATAAGTATCAATCAATCAGCCCAACTAAGTTGTCCTTTTCTGGTTTC 304

QY 1222 GTGTTTCAACATGAACATTTTGAATATAGTATTAATCTTCTATCTTGAATCTT 1273
DB 305 ATGTTCCCGTGAACATTTTGAATATAGTATTAATCTTCTATCTTGAATTTT 356

RESULT 7
LOCUS AV656454 385 bp mRNA linear EST 16-JAN-2002
DEFINITION AV656454 GLC Homo sapiens cDNA clone GICERE05 3', mRNA sequence.
ACCESSION AV656454
VERSION AV656454.1 GI:9877468
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 385)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PUBMED 11752456
COMMENT Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. .385
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GICERE05"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GLC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 21.4%; Score 273; DB 1; Length 385;
Best Local Similarity 86.2%; Pred. No. 8.2e-53;
Matches 337; Conservative 0; Mismatches 0; Indels 54; Gaps 1;

QY 883 CATGATTTCCAGGAAGCAAGATTGGCATATCATTTGTAATATAAAAGCTGACATTGACCC 942
DB 1 CATGATTTCCAGGAAGCAAGATTGGCATATCATTTGTAATATAAAAGCTGACATTGACCC 60

QY 943 AGACATATTTGTAATCTTTCTTTAAAAATAATAATAATGCTAAACAGAAAGAGAACCG 1002
DB 61 AGACATATTTGTAATCTTT-----TCTACAGCTAGTAGAGACTTTTGGAGGAAGAAATTAAGTATCATG 77

QY 1003 TTGCTTTGCAATCTACAGCTAGTAGAGACTTTTGGAGGAAGAAATTAAGTATCATG 1062
DB 78 -----TCTACAGCTAGTAGAGACTTTTGGAGGAAGAAATTAAGTATCATG 126

QY 1063 CAGTGTTCAGAGCAAGCAAGATTGAAGTTGCCCTAGACCAGAGACATAAGTATCATG 1122
DB 127 CAGTGTTCAGAGCAAGCAAGATTGAAGTTGCCCTAGACCAGAGACATAAGTATCATG 186

QY 1123 TCTCTTTTAACTAGCATACCCGAAAGTGGAGAGAGGTGCAGCAGGCTCAAAGGCATAAGT 1182
DB 187 TCTCTTTTAACTAGCATACCCGAAAGTGGAGAGAGGTGCAGCAGGCTCAAAGGCATAAGT 246

QY 1183 CATTCGAATCAGCCAACTAAGTTGCTCTTTTCTGGTTTCCGTGTTTCAACATGGAACATTTT 1242
DB 247 CATTCGAATCAGCCAACTAAGTTGCTCTTTTCTGGTTTCCGTGTTTCAACATGGAACATTTT 306

QY 1243 GATTATAGTTAATCTTCTTCTATCTTGAATCTT 1273
DB 307 GATTATAGTTAATCTTCTTCTATCTTGAATCTT 337

RESULT 8
LOCUS AQ456663 518 bp DNA linear GSS 21-APR-1999
DEFINITION HS_5166_A1_C10_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=742 Col=19 Row=E, genomic survey sequence.
ACCESSION AQ456663
VERSION AQ456663.1 GI:4591998
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 518)
AUTHORS Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 742 row: E column: 19
Seq primer: T7
Class: BAC ends
High quality sequence stop: 518.
Location/Qualifiers
1. .518
source

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/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/notes="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"

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ORIGIN

```

Query Match          15.9%; Score 203; DB 8; Length 518;
Best Local Similarity 91.0%; Pred. No. 1.8e-36;
Matches 212; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1041 GAATTCACAGGTGTCTTCAGCAGTGTTCAGAGCCCAAGCAAGATTGCAAGTTGCCTAG 1100
DB 35 GTANNCCAGCGNGNCTTCAGCAGTGTTCAGAGCCCAAGCAAGATTGCAAGTTGCTAG 94

QY 1101 ACCAGAGCATAAGTATCATGTCTCTTTAACTAGCATACCCCGAAGTGGAGAGGGTG 1160
DB 95 ACCAGATGACATTTTATCATGTCTCTTTAACTAGCATACCCCGAAGTGGAGAGGGTG 154

QY 1161 CAGCAGGCTCAAGGCAATAGTCAATCCCAATCAGCCCACTAAGTTGCTCTTTCTGGTTT 1220
DB 155 CATTACGCTCAAGGCAATAAATCATTTCCCAATCAGCCCACTAAGTTGCTCTTTCTGGTTT 214

QY 1221 CGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAATCTT 1273
DB 215 CGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAATCTT 267

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```

RESULT 9
CF106639
LOCUS
DEFINITION
  374 bp mRNA linear EST 22-JUL-2003
  ZP0304D3 Pig liver cDNA Sus scrofa cDNA clone 04D3 similar to
  Coagulation Factor IX (F9), mRNA sequence.
ACCESSION
  CF106639
VERSION
  CF106639.1 GI:33145706
KEYWORDS
  EST.
SOURCE
  Sus scrofa (pig)
  Sus scrofa
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
  Ernst,C.W., Raney,N.E., Martinez,M.M., Hargrave,K.M., Hill,G.M. and
  Link,J.E.
  Identification of differentially expressed genes in pig liver
  tissue
  Unpublished (2003)
  Contact: Ernst CW
  Animal Science Molecular Genetics Lab
  Michigan State University
  B220 Anthony Hall, East Lansing, MI 48824, USA
  Tel: 517 432 1941
  Fax: 517 353 1699
  Email: ernstc@msu.edu
PCR PRIMERS
  FORWARD: ACAATTTCACAGGAGCTAGCAGAC
  BACKWARD: ACGACTCACTATAGGCGCTTTTCTTTTATC
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Seq primer: M13F
POLYA=Yes.

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FEATURES

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ORIGIN

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Query Match          11.8%; Score 149.6; DB 7; Length 374;
Best Local Similarity 75.8%; Pred. No. 4.7e-24;
Matches 226; Conservative 0; Mismatches 64; Indels 8; Gaps 3;

QY 436 CATCAAAACACTACTCTCTTTTCTCTACCC-TATTCTCAATCTTTTACCTTTTCCAAA 494
DB 20 CATCATAAAGCTGATCTTTCTCGGTACCTTGGTCTGATCTGCTATCTTTCCCAAC 79

QY 495 TCCCAATCCCAATCAGTTTTTCTTTCTTTTACTCCCTCTCTCCCTTTTACCCTCCATG 554
DB 80 TCCTAAACCCCAAGTCAGTTTTTCTCTCTCTCTCTCCCTCCCTGCCCTTCTCTTCTTA 139

QY 555 GTCGTTAAAGGAGAGATGGGAGCATCATCTGTATATACTTCTGTACACAGTTATACATG 614
DB 140 GGCATTAAAGGAGGGAAGGGAGCATCATCTGTTTTACTGTGTACACAATGATGCAAA 199

QY 615 TCTATCAAAACCCAGACTTGTCTTCCATAGTG---GAGACTTGTCTTTTCAGAACATAGGA 670
DB 200 CCTATCAAAACCCAGCTTGTCTTCAATTTGTTCTTGGACTTCTCTTTGAGAGGTACAT 259

QY 671 TGAAGTAAGTGCCTGAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTTAAGTTATT 728
DB 260 TGAAGTAAGTGCCTGAA--CTTGGAGGAAAAGTTCTCTTTGGAGAGGTACATTATT 314

RESULT 10
BX926315
LOCUS
DEFINITION
  688 bp mRNA linear EST 07-MAY-2004
  BX926315 Sus Scrofa library (scan) Sus scrofa cDNA clone
  scan0021d.c.01 5prim, mRNA sequence.
ACCESSION
  BX926315
VERSION
  BX926315.1 GI:41143163
KEYWORDS
  EST.
SOURCE
  Sus scrofa (pig)
  Sus scrofa
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
  1 (bases 1 to 688)
  Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S.,
  Soares,M., Bonaldo,F. and Hatey,F.
  A Pig Normalised Multi-Tissue cDNA Library
  Unpublished (2003)
  Contact: Tosser-Klopp G
  Genetique Animale
  Institut National de la Recherche Agronomique
  Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
  cedex, FRANCE
  Tel: 33 (0) 5.61.28.51.14
  Fax: 33 (0) 5.61.28.53.08
  Email: tosser@toulouse.inra.fr
  Sequence cleaned of vector, adaptor and repetitions. Contact us
  at signasupport@jouy.inra.fr to obtain the chromatogram of this
  sequence.
  Plate: 0021 row: C column: 1.
  Location/Qualifiers
    1..688
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      /mol_type="mRNA"
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      /dev_stages="from embryos to adults"
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      skin, spleen, thymus, placenta, pituitary gland, seminal
      vesicle, small intestine, uterus, adrenals, bulbo urethral
      gland, cerebral trunk, epididymis, female gonad,
      gall-bladder, hippocampus, large intestine, male gonad,
      melanocytes, stomach, udder"

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Beet Local Similarity 75.8%; Pred. No. 5.1e-24;	
Matches 226; Conservative 0; Mismatches 64; Indels 8; Gaps 3;	
Qy	436 CATCAAAAACACTACTCTCTTTCTCCTCTACCC-TATTTCTCTCAATCTTTTACCTTTTCCAA 494
Db	21 CATCAGAAAGCTGCATCTTTCTCGGTACCTTGGTCTGCATCTGCTATCTTTTCCAA 80
Qy	495 TCCCAATCCCAATCATGTTTTCTCTTTCTTTACTCTCCTCTCTCTCTTTTACCTTCCATG 554
Db	81 TCCTAACCCCAAGTCAGTTTTCTCTTTCTCTCTCCCTCCTGCCCTTTTCCTTTCTTA 140
Qy	555 GTCGTTAAAGAGAGATGGGGACATCATCTGTGTATATCTCTGTACACAGTTATACATG 614
Db	141 GGCATTAAAGAGGGAAGGGGAGCATCATCTGTTTACTGCTGTACACAATGATGCAA 200
Qy	615 TCATCAAAACCAGACTTGCTTCCATAGT---GAGACTTGCTTTTCAGAAACATAGGGA 670
Db	201 CCTATCAAAACCAGCTTGTCTTTCAATTTGTTCTTGGACTTGTCTGTATAGCACTGGGA 260
Qy	671 TGAAGTAAGTGCCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTTAAGTTATT 728
Db	261 TGAAGTAAGTGCCCTGAA---CTTGGAGGAAAAGTTCTCTCTGGAGAGTCACATTTAT 315

RESULT 12	
CO775581	
LOCUS	257 bp mRNA linear EST 04-AUG-2004
DEFINITION	ILLUMIGEN MQO_52905 Katze MFUV Macaca fascicularis cDNA clone
	IBUW:29284 5' similar to Bases 5 to 157 highly similar to human F99
	(Hg.1330), mRNA sequence.
ACCESSION	CO775581
VERSION	CO775581.1 GI:50976844
KEYWORDS	EST.
SOURCE	Macaca fascicularis (crab-eating macaque)
ORGANISM	Macaca fascicularis
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
	Cercopithecinae; Macaca.
REFERENCE	1 (bases 1 to 257)
AUTHORS	Katze, M.G., Thomas, M., Iadonato, S.P. and Magnus, C.L.
TITLE	Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL	Unpublished (2003)
COMMENT	Contact: C. Magnus Illumigen Biosciences Inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400 Fax: 2063780408

```

FEATURES
source
1. .257
/organism="Macaca fascicularis"
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/strain="Indian"
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/clone="IBIUM:29284"
/dev_stage="adult"
/lab_host="Electromax DH10B"
/clone_lib="Katze MPLV"
/notes="Organ: liver; Vector: pDONR 222; Site 1: BarG I; Site 2: BarG I; Created from CloneMiner cDNA Library Construction kit (catalog #18249-029)"
Seq primer: CCCTCACTAAAGGGAACAAAA
POLYA=Yes.
Location/Qualifiers

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ORIGIN

Query Match	11.5%;	Score 147;	DB 7;	Length 257;
Best Local Similarity	93.9%;	Pred. No. 1.8e-23;	Mismatches 0;	Indels 0;
Matches 153;	Conservative	0;		
QY	567	GAGATGGGGAGCATCATCTCTGTATATCTCTGTACACAGTATACATGCTATCAAAACC	626	
DB	3	GGGATGGGGAGCATCATCTCTGTATATCTCTGTACCGAGTATACATGCTATCAAAACC	62	
QY	627	AGACTTGCTTCATAGTGAGACTTCCTTTTCAGAACATAGGATGAAGTGGCTG	686	
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QY	687	AAAAAGTTTCGGGAAAGTTTCTTTCAGAGAGTTAGTTATTT	729	
DB	123	AAATTTTGGGAAAGTTTCTTTCAGAGAGTTATATATAT	165	
RESULT 13				
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DEFINITION	SLL07a27j01f1 squirrel liver library 3			EST 29-JUL-2004
ACCESSION	CO740602			
VERSION	CO740602.1	GI:50827872		
KEYWORDS	EST.			
SOURCE	Spermophilus lateralis (golden-mantled ground squirrel)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scuriinae; Spermophilus.			
REFERENCE	1 (bases 1 to 583)			
AUTHORS	Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W., Rogers,J. and Cossins,A.R.			
TITLE	Microarray analysis of transcriptional changes during hibernation in the golden mantled ground squirrel, Spermophilus lateralis			
JOURNAL	Unpublished (2004)			
COMMENT	Contact: Andrew R. Cossins Laboratory for Environmental Gene Regulation University of Liverpool School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 7ZB Tel: +44(0)151-795-4510 Fax: +44(0)151-795-4431 Email: cossins@liv.ac.uk Vector has been trimmed from this EST. Plate: 27 row: j column: 01 Seq primer: Triplex 5'LD (5'-CTCGGAGCGCGCCATTGTGTGGT-3') High quality sequence stop: 583.			
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	/clone_lib="squirrel liver library 3"			
	/note="Vector: pTriplex2; Site 1: Sfil GGCCATTACGGCC; Site 2: Sfil GCGCGCTCGGC; Normalized cDNA library prepared from liver of hibernating and summer animals"			
ORIGIN				
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Best Local Similarity	66.3%;	Pred. No. 2.9e-17;	Matches 274;	Conservative 0;
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Gaps	6;			
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DB	120	TGATTATGGCAGTCTGGCTGGGAATGGTTCCATCAAGGCAAGGCTG---CAGGTCACTAA	176	
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DB	237	AGAA-----AGAACATCCCATTTTGCAACCAAGAACTAGCAGATTCTTTAAGGGA	285	
QY	1041	GAATTCACAGTGTGCTCTTCAGCAGTGTTCAGAGCCAGCAAGAAGTTGAAGTTGCCTAG	1100	
DB	286	GAATTCACAGCATATCTCCAACATTACCTGGAGTCNAACAA-----GAAGTTTCTTAG	339	
QY	1101	ACCAGAGACATAAGTATCATGTCTCTTTTAACTAGCATACCCGAAAGTGGAGAGGGTG	1160	
DB	340	ACCAGAAACCATGACATCATCT---CCTTGGCTAATATATACATCAGTGGAGAGGACA	396	
QY	1161	CAGCAGGCTCAAGGCATCAAGTCAATCCAAATCAGCCAACACTAAGTTGTCC-TTTTCTGGTT	1219	
DB	397	CA-CAGGCTCAAGAGCTGAGTCATTACACCCAGATAACCAACTCCCTCTTTTGTATT	455	
QY	1220	TGCTGTTCCACCATGCAATTTTGATTATAGTTAATCTCTTCTATCTTGAATCT	1272	
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RESULT 14				
LOCUS	CE730574	592 bp	DNA	linear
DEFINITION	tigr-gss-dog-17000315417737 Dog Library Canis familiaris genomic, genomic survey sequence.			
ACCESSION	CE730574			
VERSION	CE730574.1	GI:37070694		
KEYWORDS	GSS.			
SOURCE	Canis familiaris (dog)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fiesipedia; Canidae; Canis.			
REFERENCE	1 (bases 1 to 592)			
AUTHORS	Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.			
TITLE	The dog genome: survey sequencing and comparative analysis			
JOURNAL	Science 301 (5641), 1898-1903 (2003)			
MEDLINE	22875432			
PUBMED	14512627			
COMMENT	Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-0200 Fax: 301-838-0208 Email: ekirknes@tigr.org Class: shotgun.			
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Db 143 AAGTGAATTAGAAAATGTAATCACTACGGAAATGTACTGTGTAGGAACTTTGTGACCACT 84
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Db 83 CCACAGGTCTACGCCCTTGGCACCATTGTGAGGTAGGTATTTCTCTCGCCGTCAGGT 24
QY 231 ACTATGTTCTCCCACTATGSCAA 253
Db 23 GTTAAGTTTCTCCACTGGGGCAA 1

RESULT 15
CA456053
LOCUS
DEFINITION AGENCOURT_10732714 NIH_MGC_152 Mus musculus cDNA clone
IMAGE:6745686 5', mRNA sequence.
CA456053
ACCESSION CA456053.1 GI:24907345
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 816)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Bradfield Laboratory
CDNA Library Preparation: Mark Bittinger
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM00083 row: p column: 05
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FEATURES
source

1..816
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Site 2: attP1; cDNA made by oligo-dT with attB2 site and
directionally cloned. Priming sequence:
5'-TTTCTGCGAGCGCCACCTTGTACAGAAAGCTGGTTTTTTTTTTTT
TTTTT-3'. Full-length enriched library was constructed
using the GeneRacer kit by Invitrogen, library
amplification 16 cycles. Library constructed by Mark
Bittinger in the Bradfield laboratory (McArdle Laboratory
for Cancer Research, University of Wisconsin). Note: this
is a NIH_MGC Library."

ORIGIN

Query Match 7.5%; Score 95.8; DB 6; Length 816;
Best Local Similarity 56.7%; Pred. No. 1.8e-11;
Matches 316; Conservative 0; Mismatches 177; Indels 64; Gaps 5;
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QY 83 AGGGGAGAAATTC-----ATATTTTACCTGAGCAAAATGATTAGAAAATGGAAC 131

Db 290 ATAAGCAAGCCCATCTAGGATCTATATTTGTTCTAGAGTAAGTAGGTTAGCAAGATAAT 349
QY 132 CACTAGAGGAATATAATGTGTGTAGGAAATTTACAGTCAATTTCTAAGGGCCAGCCCTTGAC 191
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QY 192 AAAATTGTGAAGTTAAATTTCTCCACTCTGTCCATCAGATACTATGTGTTCTCCACTATGGC 251
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QY 432 AACTCATCAAAAACACTACTCTCTTTTCTCTACCCCTATTCTCTCAATCTTTTACCTTTCC 491
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QY 552 ATGGTCGTTTAAAGGAGA 568
Db 717 ACCACTGAAAGAGGAAA 733

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Job time : 3952 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 13:28:03 ; Search time 877 Seconds
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10022.381 Million cell updates/sec

Title: US-10-018-392A-3
Perfect score: 1273
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1273	100.0	1707	9	US-09-884-901-7
3	1273	100.0	2804	14	US-10-132-829-2
4	1273	100.0	2804	16	US-10-133-907-2
5	1273	100.0	2804	21	US-10-956-157-357
6	1273	100.0	2804	21	US-10-804-763-40
7	1273	100.0	38059	9	US-09-880-107-2125

8	1269.8	99.7	2792	9	US-09-118-748-1	Sequence 1, Appli
9	1259	98.9	2773	17	US-10-349-858-16	Sequence 16, Appli
10	1258.6	98.9	2728	21	US-10-741-600-3	Sequence 3, Appli
11	1258.6	98.9	2771	21	US-10-741-600-1	Sequence 1, Appli
12	1258.6	98.9	2777	21	US-10-741-600-2	Sequence 2, Appli
13	1258.6	98.9	2831	21	US-10-741-600-4	Sequence 4, Appli
14	1258.6	98.9	44752	21	US-10-741-600-17553	Sequence 17553, A
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16	200.6	15.8	201	21	US-10-741-600-1929	Sequence 1929, Ap
17	200.6	15.8	201	21	US-10-741-600-2210	Sequence 2210, Ap
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20	200.6	15.8	201	21	US-10-741-600-18362	Sequence 18362, A
21	186	14.6	1438	17	US-10-038-854-5	Sequence 5, Appli
22	152.6	12.0	422	9	US-09-960-352-12761	Sequence 12761, A
23	110	8.6	1610	15	US-10-073-064-6	Sequence 6, Appli
24	110	8.6	13928	18	US-10-362-916-1	Sequence 1, Appli
25	109	8.6	1548	9	US-09-150-811-6	Sequence 6, Appli
26	74.4	5.8	370	9	US-09-960-352-11540	Sequence 11540, A
27	60	4.7	60	10	US-09-908-975-8732	Sequence 8732, Ap
28	53.2	4.2	330	19	US-10-674-124A-23744	Sequence 23744, A
29	52	4.1	624	13	US-10-027-632-242636	Sequence 242636,
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31	51.8	4.1	133100	22	US-10-723-681-4	Sequence 4, Appli
32	51.2	4.0	223556	13	US-10-087-192-394	Sequence 394, App
33	51	4.0	10595	18	US-10-221-714A-264	Sequence 264, App
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35	50.6	4.0	337022	19	US-10-322-696-52	Sequence 52, Appli
36	49.8	3.9	236	19	US-10-674-124A-19594	Sequence 19594, A
37	49.6	3.9	452	19	US-10-674-124A-15774	Sequence 15774, A
38	49.6	3.9	1207	13	US-10-027-632-203235	Sequence 203235,
39	49.6	3.9	1207	17	US-10-027-632-203235	Sequence 203235,
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41	49	3.8	352	19	US-10-674-124A-15437	Sequence 15437, A
42	48.8	3.8	606	13	US-10-027-632-227381	Sequence 227381,
43	48.8	3.8	606	17	US-10-027-632-227381	Sequence 227381,
44	48.8	3.8	3256	17	US-10-264-049-770	Sequence 770, App
45	48.8	3.8	6692	18	US-10-221-714A-131	Sequence 131, App

ALIGNMENTS

RESULT 1

US-10-956-157-5592
; Sequence 5592, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH:
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE OF INVENTION: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5592
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-5592

Query Match	100.0%	Score 1273;	DB 21;	Length 1400;
Best Local Similarity	100.0%	Pred. No. 1.1e-299;		
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Qy 1201 AGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGATTATAGTTAAATCCCTTC 1260
Db 1260 AGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGATTATAGTTAAATCCCTTC 1319
Qy 1261 TATCTTGAATCTT 1273
Db 1320 TATCTTGAATCTT 1332
RESULT 2
US-09-884-901-7
; Sequence 7, Application US/09884901
; Patent No. US20020076798A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Carol
; APPLICANT: Kay, Mark
; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
; FILE REFERENCE: UOPW-1-17396
; CURRENT APPLICATION NUMBER: US/09/884,901
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,902
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1707
; TYPE: DNA
; ORGANISM: HomoSapien
US-09-884-901-7
Query Match 100.0%; Score 1273; DB 9; Length 1707;
Best Local Similarity 100.0%; Pred. No. 1.2e-299; Mismatches 0; Indels 0; Gaps 0;
Matches 1273; Conservative 0;
Qy 1 GGCCTCTCACCTAACTAACTCACTTTCCCATCTTTTGTAGATTGGAATATATACATTTCTAT 60
Db 51 GGCCTCTCACCTAACTAACTCACTTTCCCATCTTTTGTAGATTGGAATATATACATTTCTAT 110
Qy 61 GATCATTTGCTTTTCTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTA 120
Db 111 GATCATTTGCTTTTCTCTTTTACAGGGAGAAATTTTCATATTTTACCTGAGCAAAATGATTA 170
Qy 121 GAAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTTCTAAGGGCC 180
Db 171 GAAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTTCTAAGGGCC 230
Qy 181 CAGCCCTTGACAAAATTTGTGAAGTTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC 240
Db 231 CAGCCCTTGACAAAATTTGTGAAGTTTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC 290
Qy 241 TCCACTATGGCAATTAACCTCACTCAATTTTCCCTCTTACGAGCAATTCATCTTCCCGAT 300
Db 291 TCCACTATGGCAATTAACCTCACTCAATTTTCCCTCTTACGAGCAATTCATCTTCCCGAT 350
Qy 301 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATTTAGTTCTGTATACAGTACAGGATC 360
Db 351 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATTTAGTTCTGTATACAGTACAGGATC 410
Qy 361 TTTGCTTACTCTATCACAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420
Db 411 TTTGCTTACTCTATCACAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 470
Qy 421 TGAGAGGCTAAAACCTCATCAAAAACACATCTCTCTTTTCCCTTACCCCTATTCCTCAATCTT 480
Db 471 TGAGAGGCTAAAACCTCATCAAAAACACATCTCTCTTTTCCCTTACCCCTATTCCTCAATCTT 530
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTCTTTACTCCCTCTCTCCC 540
Db 531 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTTTCTTTACTCCCTCTCTCCC 590
Qy 541 TTTTACCCCTCCATGGTGGTAAAGGAGAGATGGGAGCATCATTTCTGTTATATCTCTGTA 600

591	Db	TTTTACCCCTCCATCGTTCGTTAAAGGAGAGATGGGGAGCATCATTTCTGTGTATACTTCTGTGA	650
601	Qy	CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTTCATAGTGGAGACTTGTCTTTTCAG	660
651	Db	CACAGTTATACATGCTCTATCAAAACCCAGACTTGTCTTCATAGTGGAGACTTGTCTTTTCAG	710
661	Qy	AACATAGGGATGAAGTAAAGTGCCTGAAAAAGTTTGGGGGAAAAAGTTCTTTTCAGAGAGTT	720
711	Db	AACATAGGGATGAAGTAAAGTGCCTGAAAAAGTTTGGGGGAAAAAGTTCTTTTCAGAGAGTT	770
721	Qy	AAGTTATTTTATATATATAATATATATAAATATATAAATATATAAATATATAAATATATATAG	780
771	Db	AAGTTATTTTATATATAATATATATAAATATATAAATATATAAATATATAAATATATAAATATATAG	830
781	Qy	TGTTGTGTGTATCGTGTGTGTAGACACACACCGCATACACACATATAATATGGAAGCAATA	840
831	Db	TGTTGTGTGTATCGTGTGTGTAGACACACACCGCATACACACATATAATATGGAAGCAATA	890
841	Qy	AGCCATTTCAAGAGCTTGTATGGTTATGGAGTCTGACTAGGCATGATTTTCACGAAGGCA	900
891	Db	AGCCATTTCAAGAGCTTGTATGGTTATGGAGTCTGACTAGGCATGATTTTCACGAAGGCA	950
901	Qy	AGATTGGCATATCATTTGTAACATAAAAAAGCTGCACATTTGACCCAGACATATTTGTACTCTTT	960
951	Db	AGATTGGCATATCATTTGTAACATAAAAAAGCTGCACATTTGACCCAGACATATTTGTACTCTTT	1010
961	Qy	CTAAAAATAATAATAATTAATGCTAAACAGAAGAGAGAACCGTTTCGTTTTCGAATCTACAG	1020
1011	Db	CTAAAAATAATAATAATTAATGCTAAACAGAAGAGAGAACCGTTTCGTTTTCGAATCTACAG	1070
1021	Qy	CTAGTAGAGACTTTTGAGGAAGAAATTCACACAGTGTGTCTTCAGCAGTGTTCAGAGCCCAAGC	1080
1071	Db	CTAGTAGAGACTTTTGAGGAAGAAATTCACACAGTGTGTCTTCAGCAGTGTTCAGAGCCCAAGC	1130
1081	Qy	AAGAAGTTGAAGTTGCCCTAGACACAGAGGACATAAGTATCATGTCTCCTTTAACTAGACATA	1140
1131	Db	AAGAAGTTGAAGTTGCCCTAGACACAGAGGACATAAGTATCATGTCTCCTTTAACTAGACATA	1190
1141	Qy	CCCCGAAGTGGAGAAGGGTGCACAGAGCTCAAGGGCATAGTCATTTCCATCAGCCCAACT	1200
1191	Db	CCCCGAAGTGGAGAAGGGTGCACAGAGCTCAAGGGCATAGTCATTTCCATCAGCCCAACT	1250
1201	Qy	AAGTTGTCTCTTTTCTCGTGTTCGTTTCACCATGGAACATTTTGAATATAGTTAATCTCTTC	1260
1251	Db	AAGTTGTCTCTTTTCTCGTGTTCGTTTCACCATGGAACATTTTGAATATAGTTAATCTCTTC	1310
1261	Qy	TATCTTGAATCTT	1273
1311	Db	TATCTTGAATCTT	1323

RESULT 3

RES001 3
 US-10-132-829-2
 ; Sequence 2, Application US/10132829
 ; Publication No. US20030044982A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, Kenneth R
 ; APPLICANT: Hoshijima, Masahiko
 ; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII
 ; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII
 ; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VIII
 ; FILE REFERENCE: 6627-Pall170
 ; CURRENT APPLICATION NUMBER: US/10/132,829
 ; CURRENT FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: 60/286,314
 ; PRIOR FILING DATE: 2001-04-25
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 2804
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-132-829-2

Query Match	100.0.0%;	Score 1273;	DB 14;	Length 2804;
Best Local Similarity	100.0.0%;	Pred. No. 1.5e-299;		
Matches 1273;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTCCCATCTTTTGGTTAGATTTTGAATATATACATCTCTAT	60	
Db	1464	GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTGGTTAGATTTTGAATATATACATCTCTAT	1523	
Qy	61	GATCATTTGCTTTTCTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTTGATTA	120	
Db	1524	GATCATTTGCTTTTCTCTTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTTGATTA	1583	
Qy	121	GAATAATGGAACCACTAGAGGAATATATATGTTGTAGAAATTTACAGTCATTTCTAAGGGCC	180	
Db	1584	GAATAATGGAACCACTAGAGGAATATATATGTTGTAGAAATTTACAGTCATTTCTAAGGGCC	1643	
Qy	181	CAGCCCTTGACAAAATTTGTGAGGTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC	240	
Db	1644	CAGCCCTTGACAAAATTTGTGAGGTAAATTTCTCCACTCTGTCCATCAGATACTATGGTTC	1703	
Qy	241	TCCACTATGSCAACTAACTCACTCAATTTTTCCCTCTCTTAGCAGCATTTCCATCTTCCCGAT	300	
Db	1704	TCCACTATGSCAACTAACTCACTCAATTTTTCCCTCTCTTAGCAGCATTTCCATCTTCCCGAT	1763	
Qy	301	CTTCTTTTGCTTCTCCAAACCAAAACATCAATGTTTATTTAGTTCGTATACAGTACAGATC	360	
Db	1764	CTTCTTTTGCTTCTCCAAACCAAAACATCAATGTTTATTTAGTTCGTATACAGTACAGATC	1823	
Qy	361	TTTGGTCTACTCTATCACAGGCCAGTACCACACTCATGAAAGAAACACAGAGGTAGC	420	
Db	1824	TTTGGTCTACTCTATCACAGGCCAGTACCACACTCATGAAAGAAACACAGAGGTAGC	1883	
Qy	421	TGAGAGGCTAAAACTCATCAAAAAACACTACTCTCTTTTCTCTACTACCCCTATTCTCTCAATCTT	480	
Db	1884	TGAGAGGCTAAAACTCATCAAAAAACACTACTCTCTTTTCTCTACTACCCCTATTCTCTCAATCTT	1943	
Qy	481	TTACCTTTTCCAAATCCCAATCCCAAAATCAAGTTTTTCTCTTTTCTTTACTCCCTCTCTCCC	540	
Db	1944	TTACCTTTTCCAAATCCCAATCCCAAAATCAAGTTTTTCTCTTTTCTTTACTCCCTCTCTCCC	2003	
Qy	541	TTTTACCCCTCCATGGTGGTTTAAAGAGAGATGGGGAGCATCATTTCTGTTATACTTCTGTA	600	
Db	2004	TTTTTACCCCTCCATGGTGGTTTAAAGAGAGATGGGGAGCATCATTTCTGTTATACTTCTGTA	2063	
Qy	601	CACAGTTATACATGTCCTATCAAAACCCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTTCAG	660	
Db	2064	CACAGTTATACATGTCCTATCAAAACCCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTTCAG	2123	
Qy	661	AACATAGGATGAAGTAAAGTGCCCTGAAAAGTTTGGGGAAAAGTTTCTTTTCAGAGATT	720	
Db	2124	AACATAGGATGAAGTAAAGTGCCCTGAAAAGTTTGGGGAAAAGTTTCTTTTCAGAGATT	2183	
Qy	721	AAAGTTATTTATATATATATATATATATAAATATATAATATACAAATATAATATATATAG	780	
Db	2184	AAAGTTATTTATATATATATATATATAAATATATAAATATATAATATACAAATATAATATATAG	2243	
Qy	781	TGTGTGTGTATGCGTGTGTAGACACACACGCAATACACATATAATATGGAAGCAATA	840	
Db	2244	TGTGTGTGTATGCGTGTGTAGACACACACGCAATACACATATAATATGGAAGCAATA	2303	
Qy	841	AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTTCAGAAAGGCA	900	
Db	2304	AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTTCAGAAAGGCA	2363	
Qy	901	AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT	960	
Db	2364	AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTTGACCCAGACATATTTGACTCTTTT	2423	
Qy	961	CTAAAAATAATATAATATGCTTAACAGAAAGAGAACCCGTTCCGTTTGCATCTACAG	1020	
Db	2424	CTAAAAATAATATAATATGCTTAACAGAAAGAGAACCCGTTCCGTTTGCATCTACAG	2483	
Qy	1021	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTGTCTTTTCAGCAGTGTGTTTCAGAGCCNAGC	1080	

Db	2484	CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGCTTCAGCAGGTTCAGAGCCAAGC	2543	
Qy	1081	AGAAAGTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTAACTAGCAT	1140	
Db	2544	AGAAAGTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTAACTAGCAT	2603	
Qy	1141	CCCCGAAGTGGAGAGGGTGACAGGCTCAAGAGGATTAAGTCAATCCAAATCAGCCAAT	1200	
Db	2604	CCCCGAAGTGGAGAGGGTGACAGGCTCAAGAGGATTAAGTCAATCCAAATCAGCCAAT	2663	
Qy	1201	AAGTTGCTCTTTCTCGTTTCGTTTCCCATGGAAATTTTGAATATATGTTAATCCTTC	1260	
Db	2664	AAGTTGCTCTTTCTCGTTTCGTTTCCCATGGAAATTTTGAATATATGTTAATCCTTC	2723	
Qy	1261	TATCTTGAATCTT	1273	
Db	2724	TATCTTGAATCTT	2736	
RESULT 4				
US-10-133-907-2				
; Sequence 2, Application US/10133907				
; Publication No. US20030195223A1				
; GENERAL INFORMATION:				
; APPLICANT: Chien, Kenneth R				
; APPLICANT: Hoshijima, Masahiko				
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII				
; TITLE OF INVENTION: with vesicle vector				
; FILE REFERENCE: 6627-PAL170				
; CURRENT FILING DATE: 2002-04-25				
; PRIOR APPLICATION NUMBER: 60/286,314				
; PRIOR FILING DATE: 2001-04-25				
; NUMBER OF SEQ ID NOS: 5				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 2				
; LENGTH: 2804				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-133-907-2				
Query Match 100.0%; Score 1273; DB 16; Length 2804;				
Best Local Similarity 100.0%; Pred. No. 1.5e-299;				
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTAGATTGGAATATATACATTTCTAT	60	
Db	1464	GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTAGATTGGAATATATACATTTCTAT	1523	
Qy	61	GATCATTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA	120	
Db	1524	GATCATTGCTTTTCTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA	1583	
Qy	121	GAATAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTAAGTCATTTCTTAAGGGCC	180	
Db	1584	GAATAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTAAGTCATTTCTTAAGGGCC	1643	
Qy	181	CAGCCCTTGACAAAATTTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTTC	240	
Db	1644	CAGCCCTTGACAAAATTTGAAGTTAAATTTCTCCACTCTGTCCATCAGATCTATGGTTTC	1703	
Qy	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCTATCTCCGAT	300	
Db	1704	TCCACTATGGCACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCTATCTCCGAT	1763	
Qy	301	CTTCTTTGCTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	360	
Db	1764	CTTCTTTGCTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	1823	
Qy	361	TTTGGTCTACTCTATCACAAGGCCAGTACACACTCATGAAGAAAGAACACAGGAGTAGC	420	
Db	1824	TTTGGTCTACTCTATCACAAGGCCAGTACACACTCATGAAGAAAGAACACAGGAGTAGC	1883	

Qy	421	TGAGAGGCTAAATCTCATCAAAAAACACTACTCCTTTTCTCTACCCCTATTCTCTCAATCTT	480	
Db	1884	TGAGAGGCTAAATCTCATCAAAAAACACTACTCCTTTTCTCTACCCCTATTCTCTCAATCTT	1943	
Qy	481	TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTCTTTTCTTACTCCCTCTCTCCC	540	
Db	1944	TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTCTTTTCTTACTCCCTCTCTCCC	2003	
Qy	541	TTTTTACCCTCCATGTGTCGTTTAAAGAGAGATGGGGAGCATCATCTCTGTATATCTTCTGTA	600	
Db	2004	TTTTTACCCTCCATGTGTCGTTTAAAGAGAGATGGGGAGCATCATCTCTGTATATCTTCTGTA	2063	
Qy	601	CACAGTTATACATGTCATATCAAAACCCAGACTTGTCTTCCATAGTGAGACTTGTCTTTTTCAG	660	
Db	2064	CACAGTTATACATGTCATATCAAAACCCAGACTTGTCTTCCATAGTGAGACTTGTCTTTTTCAG	2123	
Qy	661	AACATAGGGATGAAGTAAAGTGCCTGAAAAAGTTTGGGGGAAAAAGTTTCTTTTCAGAGAGTT	720	
Db	2124	AACATAGGGATGAAGTAAAGTGCCTGAAAAAGTTTGGGGGAAAAAGTTTCTTTTCAGAGAGTT	2183	
Qy	721	AAGTTATTTTATATATATATATATATATATAATAATAATAATAATAATAATAATAATAATA	780	
Db	2184	AAGTTATTTTATATATATATATATATATATAATAATAATAATAATAATAATAATAATAATA	2243	
Qy	781	TGTGTGTGTATGCTGTGTGTAGACACACACGACATACACATATATAATGGAAGCAATA	840	
Db	2244	TGTGTGTGTATGCTGTGTGTAGACACACACGACATACACATATATAATGGAAGCAATA	2303	
Qy	841	AGCCATTCTAAGAGCTTGTATGGAGTCTGACTAGGCGATGATTTTCACGAAGGCA	900	
Db	2304	AGCCATTCTAAGAGCTTGTATGGAGTCTGACTAGGCGATGATTTTCACGAAGGCA	2363	
Qy	901	AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTTGACCCAGACATATTTGTACTCTTT	960	
Db	2364	AGATTGGCATATCATTTGTAACCTAAAAAGCTGACATTTGACCCAGACATATTTGTACTCTTT	2423	
Qy	961	CTAAAAATAATAATAATAATCTAAACAGAAAGAGAACCGTTCGTTTGCAATCTACAG	1020	
Db	2424	CTAAAAATAATAATAATAATCTAAACAGAAAGAGAACCGTTCGTTTGCAATCTACAG	2483	
Qy	1021	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAGC	1080	
Db	2484	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAGC	2543	
Qy	1081	AGAAAGTTGAAGTTTCCCTAGACGAGGACATTAAGTATCATGTCTCTTTTAACTAGCAT	1140	
Db	2544	AGAAAGTTGAAGTTTCCCTAGACGAGGACATTAAGTATCATGTCTCTTTTAACTAGCAT	2603	
Qy	1141	CCCCGAAGTGGAGAGGGTGACAGGCTCAAAAGGCATAAAGTCATTCCCAATCAGCCAAT	1200	
Db	2604	CCCCGAAGTGGAGAGGGTGACAGGCTCAAAAGGCATAAAGTCATTCCCAATCAGCCAAT	2663	
Qy	1201	AAGTTGTCTCTTTTCTGGTTTCTGTTTCCACATGGAACATTTTGTATTAGTTAAATCCTTC	1260	
Db	2664	AAGTTGTCTCTTTTCTGGTTTCTGTTTCCACATGGAACATTTTGTATTAGTTAAATCCTTC	2723	
Qy	1261	TATCTTGAATCTT	1273	
Db	2724	TATCTTGAATCTT	2736	

RESULT 5

US-10-956-157-357
; Sequence 357, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157

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; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 357
; LENGTH: 2804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-357

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Query Match      100.0%; Score 1273; DB 21; Length 2804;
Best Local Similarity 100.0%; Pred. No. 1.5e-299;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	GGCCTCTCACTAACTAAATCACTTTCCCACTCTTTTGGTAGATTGGAATATATACATTTCTAT	60
Db	1464	GGCCTCTCACTAACTAAATCACTTTCCCACTCTTTTGGTAGATTGGAATATATACATTTCTAT	1523
Qy	61	GATCATTTGCTTTTCTCTTTTACGGGGAGAAATTCATATTTTACCTCGAGCAAAATTGATTA	120
Db	1524	GATCATTTGCTTTTCTCTTTTACGGGGAGAAATTCATATTTTACCTCGAGCAAAATTGATTA	1583
Qy	121	GAAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCAATTTCTAAGGCC	180
Db	1584	GAAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCAATTTCTAAGGCC	1643
Qy	181	CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCCACTCTGTCCATCAGATACTATGGTTC	240
Db	1644	CAGCCCTTGACAAAATTTGTGAAGTTAAATTTCCACTCTGTCCATCAGATACTATGGTTC	1703
Qy	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTTAGCAGCAATTTCCATCTTCCCGAT	300
Db	1704	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTTTAGCAGCAATTTCCATCTTCCCGAT	1763
Qy	301	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTGTTTATTAGTTCTGTATACAGTACAGATC	360
Db	1764	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTGTTTATTAGTTCTGTATACAGTACAGATC	1823
Qy	361	TTTGGTCTACTCTATCAAGGCCAGTACCACTCATGAAGAAGAAACACAGGAGTAGC	420
Db	1824	TTTGGTCTACTCTATCAAGGCCAGTACCACTCATGAAGAAGAAACACAGGAGTAGC	1883
Qy	421	TGAGAGGCTAAAACCTCATCAAAAAACATCTCTCTTTTCTCTACCTTATTCCTCAATCTTT	480
Db	1884	TGAGAGGCTAAAACCTCATCAAAAAACATCTCTCTTTTCTCTACCTTATTCCTCAATCTTT	1943
Qy	481	TTACTCTTTTCCAAATCCCAATCCCAAAATCAGTTTCTCTCTTCTACTCCCTCTCTCCC	540
Db	1944	TTACTCTTTTCCAAATCCCAATCCCAAAATCAGTTTCTCTCTTCTACTCCCTCTCTCCC	2003
Qy	541	TTTTTACCCTCCATGGTGGTTAAAGGAGAGATGGGGAGCATCATTTCTGTATATCTTGTGA	600
Db	2004	TTTTTACCCTCCATGGTGGTTAAAGGAGAGATGGGGAGCATCATTTCTGTATATCTTGTGA	2063
Qy	601	CACAGTTTATACATGTCTATCAAAACCCAGACTTGTCTCCATAGTGGAGACTTGTCTTTTCAG	660
Db	2064	CACAGTTTATACATGTCTATCAAAACCCAGACTTGTCTCCATAGTGGAGACTTGTCTTTTCAG	2123
Qy	661	AACATAGGGATGAAGTAAGTGCCGTGAAGTTTGGGGGAAAAAGTTTCTTTTCAGAGATTT	720
Db	2124	AACATAGGGATGAAGTAAGTGCCGTGAAGTTTGGGGGAAAAAGTTTCTTTTCAGAGATTT	2183
Qy	721	AAGTTATTTTATATATATATATATATAATAATATATAATACAAATATAAAATATATAG	780
Db	2184	AAGTTATTTTATATATATATATATATAATAATATATAATACAAATATAAAATATATAG	2243
Qy	781	TGTTGTGTGTATGTCGTGTGTGTAGACACACACCGCATACACATATAAATGGAAGCAATA	840
Db	2244	TGTTGTGTGTATGTCGTGTGTGTAGACACACACCGCATACACATATAAATGGAAGCAATA	2303
Qy	841	AGCCATCTTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCAATGATTTTCACGAAGCA	900
Db	2304	AGCCATCTTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCAATGATTTTCACGAAGCA	2363

9. T. J. S. A.

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RES001.8
US-10-804-763-40
; Sequence 40, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804, 763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 2804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-763-40

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Query Match	100.0%;	Score 1273	DB 21;	Length 2804;
Best Local Similarity	100.0%;	Pred. No. 1.5e-299;		
Matches 1273;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GGCCTCTCACTAACTCACTTCCCATCTTTGTTAGATTTTGAATATATACATTCCTAT	60	
Db	1464	GGCCTCTCACTAACTCACTTCCCATCTTTGTTAGATTTGAATATATACATTCCTAT	1523	
Qy	61	GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTCGATTA	120	
Db	1524	GATCATTTGCTTTTCTCTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAAAATTCGATTA	1583	
Qy	121	GAAATGGAAACCACTAGAGGAATATATGTGTTAGGAAATACAGTCATTTCTAAGGGCC	180	
Db	1584	GAAATGGAAACCACTAGAGGAATATATGTGTTAGGAAATACAGTCATTTCTAAGGGCC	1643	
Qy	181	CAGCCCTTGACAAAATTGTCAAGTTAAATTTCTCCACTCTGTCATCAGATCTATGTTTC	240	
Db	1644	CAGCCCTTGACAAAATTGTCAAGTTAAATTTCTCCACTCTGTCATCAGATCTATGTTTC	1703	
Qy	241	TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTTCCCATCTTCCCGAT	300	

Db 1704 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTTAGCAGCATTCATCTTCCCGAT 1763
Qy 301 CTTCTTTGCTTCTCCACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGATC 360
Db 1764 CTTCTTTGCTTCTCCACCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGATC 1823
Qy 361 TTTGGTCTACTCTATCACAGGCGCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 420
Db 1824 TTTGGTCTACTCTATCACAGGCGCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGC 1883
Qy 421 TGAGAGGCTAAACTCATCAAAACACTACTCTCTTTTCTCTACCCCTATTCTCTCAATCTT 480
Db 1884 TGAGAGGCTAAACTCATCAAAACACTACTCTCTTTTCTCTACCCCTATTCTCTCAATCTT 1943
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC 540
Db 1944 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC 2003
Qy 541 TTTTACCTCCATGGTCTGTTAAAGGAGAGATGGGAGCATCATCTCTTTATATCTCTGTA 600
Db 2004 TTTTACCTCCATGGTCTGTTAAAGGAGAGATGGGAGCATCATCTCTTTATATCTCTGTA 2063
Qy 601 CACAGTTATACATGCTCTATCAAAACCCAGACTTCTCTTCCATAGTGGAGACTTCTTTTCAG 660
Db 2064 CACAGTTATACATGCTCTATCAAAACCCAGACTTCTCTTCCATAGTGGAGACTTCTTTTCAG 2123
Qy 661 AACATAGGAGTGAAGTGAAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTTTCAGAGATT 720
Db 2124 AACATAGGAGTGAAGTGAAGTGCCTGAAAGTTTGGGGGAAAGTTTCTTTTCAGAGATT 2183
Qy 721 AAGTTATTTATATATATATATATATAAATAATATATAATATACAAATATAATATATAG 780
Db 2184 AAGTTATTTATATATATATATATAAATAATATATAATATATAATATATAATATATAG 2243
Qy 781 TGTGTGTGTATGCGTGTGTAGACACACACGATACACATATAATGGAAGCAATA 840
Db 2244 TGTGTGTGTATGCGTGTGTAGACACACACGATACACATATAATGGAAGCAATA 2303
Qy 841 AGCCATCTTAAGAGCTTGATGTTTATGAGGTCTGACTAGGATGATTCAGAAAGGCA 900
Db 2304 AGCCATCTTAAGAGCTTGATGTTTATGAGGTCTGACTAGGATGATTCAGAAAGGCA 2363
Qy 901 AGATTGGCATATCATTTGTAACATAAAAGCTGACATTTGACCCAGACATATTGACTCTTT 960
Db 2364 AGATTGGCATATCATTTGTAACATAAAAGCTGACATTTGACCCAGACATATTGACTCTTT 2423
Qy 961 CTAATAATATAATAATGCTTAACAGAAAGAGAACCGTTTCTGTTGCAATCTACAG 1020
Db 2424 CTAATAATATAATAATGCTTAACAGAAAGAGAACCGTTTCTGTTGCAATCTACAG 2483
Qy 1021 CTAGTAGAGACTTTGAGGAAGAAATCAACAGTGTGCTTCAGCAGTGTTCAGAGCCAAGC 1080
Db 2484 CTAGTAGAGACTTTGAGGAAGAAATCAACAGTGTGCTTCAGCAGTGTTCAGAGCCAAGC 2543
Qy 1081 AAGAAGTTGAAGTTGCTTAGACAGAGGACATAGTATCATGTCCTCTTTTAAGTACGATA 1140
Db 2544 AAGAAGTTGAAGTTGCTTAGACAGAGGACATAGTATCATGTCCTCTTTTAAGTACGATA 2603
Qy 1141 CCCCAGGTGGAGAGGGTGCAGCAGGCTCAAAAGGCATTAAGTCAATCCCAATCAGCCAATC 1200
Db 2604 CCCCAGGTGGAGAGGGTGCAGCAGGCTCAAAAGGCATTAAGTCAATCCCAATCAGCCAATC 2663
Qy 1201 AAGTTGCTCTTTCTGTTCTGTTTCCATGGAACATTTTGAATATAGTTAATCCTTC 1260
Db 2664 AAGTTGCTCTTTCTGTTTCCATGGAACATTTTGAATATAGTTAATCCTTC 1260
Qy 1261 TATCTTGAATCTT 1273
Db 2724 TATCTTGAATCTT 2736

; Sequence 2125, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2125
; LENGTH: 38059
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 K02402
US-09-880-107-2125

Query Match 100.0%; Score 1273; DB 9; Length 38059;
Best Local Similarity 100.0%; Pred. No. 5.4e-299;
Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCCTCTCACTAACCTAATCACTTTCCCATCTTTTGTAGATTGAAATATATACATTTCTAT 60
Db 34383 GGCCTCTCACTAACCTAATCACTTTCCCATCTTTTGTAGATTGAAATATATACATTTCTAT 34442
Qy 61 GATCATTTGCTTTTCTTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATGATTA 120
Db 34443 GATCATTTGCTTTTCTTTTACAGGGGAGAAATTCATATTTTACCTGAGCAAAATGATTA 34502
Qy 121 GAAATGGAACCACTAGAGGAATATAATGTTTAGGAAATACAGTCATTTCTAGGGCC 180
Db 34503 GAAATGGAACCACTAGAGGAATATAATGTTTAGGAAATACAGTCATTTCTAGGGGCC 34562
Qy 181 CAGCCCTTGACAAAATTTGTAAGTTTAAATTTCTCCTCTGTCACATCAGATCTATGTTTC 240
Db 34563 CAGCCCTTGACAAAATTTGTAAGTTTAAATTTCTCCTCTGTCACATCAGATCTATGTTTC 34622
Qy 241 TCCACTATGGCAACTTAACCTCACTCAATTTTCCCTCTTAGCAGCAATTCATCTTCCCGAT 300
Db 34623 TCCACTATGGCAACTTAACCTCACTCAATTTTCCCTCTTAGCAGCAATTCATCTTCCCGAT 34682
Qy 301 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
Db 34683 CTTCTTTGCTTCTCCAAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 34742
Qy 361 TTTGTCTACTCTATCACAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTAGC 420
Db 34743 TTTGTCTACTCTATCACAGGCCAGTACCACACTCATGAAGAAAGAACACAGAGTAGC 34802
Qy 421 TGAGAGGCTAAAACTCATCAAAAAACACTACTCTCTTTTCTCTTACCCCTATTCCTCAATCTT 480
Db 34803 TGAGAGGCTAAAACTCATCAAAAAACACTACTCTCTTTTCTCTTACCCCTATTCCTCAATCTT 34862
Qy 481 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC 540
Db 34863 TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCC 34922
Qy 541 TTTTACCTCCATGGTCTGTTAAAGGAGAGATGGGAGCATCATCTGTTATATCTTCTGTA 600
Db 34923 TTTTACCTCCATGGTCTGTTAAAGGAGAGATGGGAGCATCATCTGTTATATCTTCTGTA 34982
Qy 601 CACAGTTATACATGCTATCAAAACCCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTTCAG 660
Db 34983 CACAGTTATACATGCTATCAAAACCCAGACTTGTCTTCCATAGTGGAGACTTGTCTTTTCAG 35042

Db	2472	CTAGTAGAGACTTTGAGGAGNATTCACAGTGTGTCTTCAACAGTGTTCAGAGCCAAAGC	2531
Qy	1081	AAGAAGTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTAACTAGCATA	1140
Db	2532	AAGAAGTTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTAACTAGCATA	2591
Qy	1141	CCCCGAAGTGGAGAGGGTGCACAGGCTCAAGGCGATTAAGTATCATGTCTCTTTAACTAGCATA	1200
Db	2592	CCCCGAAGTGGAGAGGGTGCACAGGCTCAAGGCGATTAAGTATCATGTCTCTTTAACTAGCATA	2651
Qy	1201	AAGTTGTCTCTTTTCTGTTTCTGTTTCCACCATGGAACATTTTGAATATAGTTAACTCCTTC	1260
Db	2652	AAGTTGTCTCTTTTCTGTTTCTGTTTCCACCATGGAACATTTTGAATATAGTTAACTCCTTC	2711
Qy	1261	TATCTTGAATCTT	1273
Db	2712	TATCTTGAATCTT	2724
RESULT 9			
US-10-349-858-16			
; Sequence 16, Application US/10349858			
; Publication No. US20030220247A1			
; GENERAL INFORMATION:			
; APPLICANT: The Children's Hospital of Philadelphia			
; APPLICANT: HIGH, KATHERINE A.			
; APPLICANT: CAMIRE, RODNEY M.			
; APPLICANT: LARSON, PETER J.			
; APPLICANT: STAFFORD, DARREL W.			
; TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT C			
; FILE REFERENCE: 018743-0301425			
; CURRENT APPLICATION NUMBER: US/10/349,858			
; CURRENT FILING DATE: 2003-01-22			
; PRIOR APPLICATION NUMBER: 09/526,947			
; PRIOR FILING DATE: 2000-03-16			
; PRIOR APPLICATION NUMBER: 60/124,609			
; PRIOR FILING DATE: 1999-03-16			
; NUMBER OF SEQ ID NOS: 22			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 16			
; LENGTH: 2773			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-349-858-16			
Query Match 98.9%; Score 1259; DB 17; Length 2773;			
Best Local Similarity 99.8%; Pred. No. 4e-296;			
Matches 1271; Conservative 0; Mismatches 0; Indels 2; Gaps 1;			
Qy	1	GGCCTCTCACTAACTAATCACTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT	60
Db	1435	GGCCTCTCACTAACTAATCACTTCCCATCTTTTGTAGATTTGAATATATACATTTCTAT	1494
Qy	61	GATCATTTCTTTCTCTTACAGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA	120
Db	1495	GATCATTTCTTTCTCTTACAGGGAGAAATTCATATTTTACCTGAGCAAAATTGATTA	1554
Qy	121	GAATAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTTCTTAAGGGCC	180
Db	1555	GAATAATGGAAACCACTAGAGGAATATAATGTGTAGGAAATTTACAGTCATTTCTTAAGGGCC	1614
Qy	181	CAGCCCTTGACAAAATTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATCATATGGTTTC	240
Db	1615	CAGCCCTTGACAAAATTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATCATATGGTTTC	1674
Qy	241	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTCTAGCAGCATTTCCATCTTCCCGAT	300
Db	1675	TCCACTATGGCACTAACTCACTCAATTTTCCCTCTCTAGCAGCATTTCCATCTTCCCGAT	1734
Qy	301	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	360

Db	1735	CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC	1794
Qy	361	TTTGTCTTACTCTATCACAAGGCCAGTACCACACTCATGTAAGAAAGAAACACAGAGATGAC	420
Db	1795	TTTGTCTTACTCTATCACAAGGCCAGTACCACACTCATGTAAGAAAGAAACACAGAGATGAC	1854
Qy	421	TGAGAGGGCTAAACACTCATCAAAACACACTACTCTCTTTTCTCTACCTTATTCCTCAATCTT	480
Db	1855	TGAGAGGGCTAAACACTCATCAAAACACACTACTCTCTTTTCTCTACCTTATTCCTCAATCTT	1914
Qy	481	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT	540
Db	1915	TTACCTTTTCCAAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT	1974
Qy	541	TTTTTACCCTTCATGTCGTTTAAAGAGAGATGGGGAGCATCATTTCTGTTTATCTTCTGTA	600
Db	1975	TTTTTACCCTTCATGTCGTTTAAAGAGAGATGGGGAGCATCATTTCTGTTTATCTTCTGTA	2034
Qy	601	CACAGTTATACATGTCATCAAAACCCAGCTTGTCTTCCATAGTGAGACTTGTCTTTTCAG	660
Db	2035	CACAGTTATACATGTCATCAAAACCCAGCTTGTCTTCCATAGTGAGACTTGTCTTTTCAG	2094
Qy	661	AACATAGGGATGAAGTAAAGTCCCTGAAAGAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTT	720
Db	2095	AACATAGGGATGAAGTAAAGTCCCTGAAAGAGTTTGGGGGAAAAGTTTCTTTTCAGAGAGTT	2154
Qy	721	AAGTTATTTTATATATATAATATAATATAATATAATATAATATAATATAATATAATATAAT	780
Db	2155	AAGTTATTTTATATATAATATAATATAATATAATATAATATAATATAATATAATATAAT	2214
Qy	781	TGT	840
Db	2215	TGT	2274
Qy	841	AGCCATTCTTAAGAGCTTCTGTATGGAGTCTGACTAGGCGATGATTTTTCACGAAGGCA	900
Db	2275	AGCCATTCTTAAGAGCTTCTGTATGGAGTCTGACTAGGCGATGATTTTTCACGAAGGCA	2334
Qy	901	AGATTGGCATATCATTTGTAACCTAAAGAGCTGACATTCGACCCAGACATATTTGTACTCTTT	960
Db	2335	AGATTGGCATATCATTTGTAACCTAAAGAGCTGACATTCGACCCAGACATATTTGTACTCTTT	2394
Qy	961	CTAAAAATAATAATAATGCTTACAGAAAGAGAGAACCGTTCGTTTGAATCTACAG	1020
Db	2395	CT--AAATAATAATAATGCTTACAGAAAGAGAGAACCGTTCGTTTGAATCTACAG	2452
Qy	1021	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAGC	1080
Db	2453	CTAGTAGAGACTTTTGAGGAAGAAATTCACAGTGTGTCTTTCAGCAGTGTTCAGAGCCAAGC	2512
Qy	1081	AAGAAATTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTTAACTAGCATA	1140
Db	2513	AAGAAATTGAAGTTGCTTAGACAGAGGACATTAAGTATCATGTCTCTTTTAACTAGCATA	2572
Qy	1141	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAGGCGATTAAGTATCATGTCTCTTTTAACTAGCATA	1200
Db	2573	CCCCGAAGTGGAGAGGGTGCAGCAGGCTCAAGGCGATTAAGTATCATGTCTCTTTTAACTAGCATA	2632
Qy	1201	AAGTTGTCTCTTTTCTGTTTCTGTTTCCACCATGGAACATTTTGTATTAGTTAACTCCTTC	1260
Db	2633	AAGTTGTCTCTTTTCTGTTTCTGTTTCCACCATGGAACATTTTGTATTAGTTAACTCCTTC	2692
Qy	1261	TATCTTGAATCTT	1273
Db	2693	TATCTTGAATCTT	2705

RESULT 10
US-10-741-600-3
; Sequence 3, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.

```

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU004499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(2728)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-3

Query Match          98.9%;   Score 1258.6;   DB 21;   Length 2728;
Best Local Similarity 99.8%;   Pred. No. 4.9e-296;
Matches 1270;   Conservative 1;   Mismatches 0;   Indels 2;   Gaps 1;

Qy  1  GGCCTCTCAGTAACATCACTTTCCCATCTTTTGTAGATTTTGAATATATACATCTCTAT 60
Db  1390  GGCCTCTCAGTAACATCACTTTCCCATCTTTTGTAGATTTTGAATATATACATCTCTAT 1449

Qy  61  GATCAATTCCTTTTCTTTTACAGGGAGAAATTCATATTTTACCTGAGCAAAATTTGATTA 120
Db  1450  GATCAATTCCTTTTCTTTTACAGGGAGAAATTCATATTTTACCTGAGCAAAATTTGATTA 1509

Qy  121  GAAATGGAAACCACTAGAGGAATAATGTTGTAGGAAATTTACAGTCATTTCTTAAGGGCC 180
Db  1510  GAAATGGAAACCACTAGAGGAATAATGTTGTAGGAAATTTACAGTCATTTCTTAAGGGCC 1569

Qy  181  CAGCCCTTGACAAAATTTGGAAGTAAATTTCTCCACTCTCTCCATCAGACTATATGGTTC 240
Db  1570  CAGCCCTTGACAAAATTTGGAAGTAAATTTCTCCACTCTCTCCATCAGACTATATGGTTC 1629

Qy  241  TCCACTATGGCACTAATCACTCAATTTTCCCTCCTTAGCAGGATTCATCTCCCGAT 300
Db  1630  TCCACTATGGCACTAATCACTCAATTTTCCCTCCTTAGCAGGATTTCCATCTCCCGAT 1689

Qy  301  CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCGTATACAGTACAGATC 360
Db  1690  CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCGTATACAGTACAGATC 1749

Qy  361  TTTGGTCTACTATATCAAGAGGCAGTACCACTCATATGAAGAAGAACACAGGAGTAGC 420
Db  1750  TTTGGTCTACTATATCAAGAGGCAGTACCACTCATATGAAGAAGAACACAGGAGTAGC 1809

Qy  421  TGAGAGGCTAAACTCATCAAAACACTACTCTCTTTTCCCTACCCCTATTTCCTCAATCTT 480
Db  1810  TGAGAGGCTAAACTCATCAAAACACTACTCTCTTTTCCCTACCCCTATTTCCTCAATCTT 1869

Qy  481  TTACTCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 540
Db  1870  TTACTCTTTTCCAAATCCCAATCCCAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCC 1929

Qy  541  TTTTACCCCTCCATGGTGGTTAAAGGAGAGATGGGAGAGATCATCTCTGTTATATCTCTGTA 600
Db  1930  TTTTACCCCTCCATGGTGGTTAAAGGAGAGATGGGAGAGATCATCTCTGTTATATCTCTGTA 1989

Qy  601  CACAGTTATATACATGCTCTATCAAAACCCAGACTGCTTCCATAGTGGAGACTTGGCTTTCAG 660
Db  1990  CACAGTTATATACATGCTCTATCAAAACCCAGACTGCTTCCATAGTGGAGACTTGGCTTTCAG 2049

Qy  661  AACATAGGGATGAAGTAAAGGTGGCTCAAAAAGTTTGGGGGAAAAAGTTTCTTTTCAGAGAGTT 720
Db  2050  AACATAGGGATGAAGTAAAGGTGGCTCAAAAAGTTTGGGGGAAAAAGTTTCTTTTCAGAGAGTT 2109

Qy  721  AAGTTATTTTATATATATATATATATAATAAATATATAATAATATATAAATATATAATATAG 780
Db  2110  AAGTTATTTTATATATATATATATATAATAAATATATAATAATATATAAATATATAATATAG 2168

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Qy	781	TGCTGTGTGTATGCTGTGTGTATAGACACACACGCATACACATATAATATGGAAGCAATA	840
Db	2169	-GTGTGTGTGTATGCTGTGTGTATAGACACACACGCATACACATATAATATGGAAGCAATA	2227
Qy	841	AGCCATTCTTAAGAGCTTGTATGTTATGGAAGTCTGACTAGGCATGATTTTCAAGAGGCA	900
Db	2228	AGCCATTCTTAAGAGCTTGTATGTTATGGAAGTCTGACTAGGCATGATTTTCAAGAGGCA	2287
Qy	901	AGATTGGCATATCAATTGTAATACTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT	960
Db	2288	AGATTGGCATATCAATTGTAATACTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT	2347
Qy	961	CTAAAAATAATAATAATAATGCTTAACAGAAAGAGAACCGTTCGTTTCCAATCTACAG	1020
Db	2348	CTAAAAATAATAATAATAATGCTTAACAGAAAGAGAACCGTTCGTTTCCAATCTACAG	2407
Qy	1021	CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTCAGCAGTGTTCAGAGCCNAGC	1080
Db	2408	CTAGTAGAGACTTTGAGGAAGAAATTCACAGTGTGTCTTCAGCAGTGTTCAGAGCCNAGC	2467
Qy	1081	AAGAAGTTGAAGTTGCCCTAGACCAGAGGACATTAAGTATCATGTCTCTTTTAACCTAGCATA	1140
Db	2468	AAGAAGTTGAAGTTGCCCTAGACCAGAGGACATTAAGTATCATGTCTCTTTTAACCTAGCATA	2527
Qy	1141	CCCCGAAGTGGAGAAGGTCGACAGGCTCAAAAGGCATAAGTCATTCCAATCAGCCAACT	1200
Db	2528	CCCCGAAGTGGAGAAGGTCGACAGGCTCAAAAGGCATAAGTCATTCCAATCAGCCAACT	2587
Qy	1201	AAGTTGTCCCTTTCTCGTTTCGTTTCACCATGGAACATTTTGAATTATAGTTAATCCCTTC	1260
Db	2588	AAGTTGTCCCTTTCTCGTTTCGTTTCACCATGGAACATTTTGAATTATAGTTAATCCCTTC	2647
Qy	1261	TATCTTGAATCTT	1273
Db	2648	TATCTTGAATCTT	2660
RESULT 11			
US-10-741-600-1			
; Sequence 1, Application US/10741600			
; Publication No. US20050026169A1			
; GENERAL INFORMATION:			
; APPLICANT: CARGILL, Michele et al.			
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH			
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES TH			
; FILE REFERENCE: CL001499			
; CURRENT APPLICATION NUMBER: US/10/741,600			
; CURRENT FILING DATE: 2003-12-22			
; NUMBER OF SEQ ID NOS: 73997			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 2771			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; LOCATION: (1)..(2771)			
; OTHER INFORMATION: n = A, T, C or G, or insertion/deletion polymorphism (see "			
US-10-741-600-1			
Query Match 98.9%; Score 1258.6; DB 21; Length 2771;			
Best Local Similarity 99.8%; Pred. No. 5e-296;			
Matches 1270; Conservative 1; Mismatches 0; Indels 2; Gaps 1;			
Qy	1	GGCCTCTCACTAATACTCACTTCCCATCTTTGTTAGATTGGAATATATACATTCTAT	60
Db	1433	GGCCTCTCACTAATACTCACTTCCCATCTTTGTTAGATTGGAATATATACATTCTAT	1492
Qy	61	GATCATTGCTTTTCTCTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAATTCATT	120
Db	1493	GATCATTGCTTTTCTCTTTACAGGGGAGAAATTTTCATATTTTACCTGAGCAATTCATT	1552
Qy	121	GAAAAATGGAACTAGAGGAATATTAATGTGTTAGGAAATTTACAGTCATTTCTTAAGGGCC	180

1553 GAAATGGAACCACTAGAGGAATATAATGTTAGGAATACAGTCAATTTCTAAGGGCC 1612
181 CAGCCCTTGACAAAATGTGAAGTTAAATCTCCACTCTGTCCATCAGATACATATGTTTC 240
1613 CAGCCCTTGACAAAATGTGAAGTTAAATCTCCACTCTGTCCATCAGATACATATGTTTC 1672
241 TCCACTATGCGCACTAACTCACTCAATTTTCCCTCTAGCAGCATTCCTCCGAT 300
1673 TCCACTATGCGCACTAACTCACTCAATTTTCCCTCTAGCAGCATTCCTCCGAT 1732
301 CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGATC 360
1733 CTTCTTTGCTTCTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGATC 1792
361 TTTGGTCTACTCTATCACAAGGCGATGACACACTCATGAAGAAAGAAACACAGGATAGC 420
1793 TTTGGTCTACTCTATCACAAGGCGATGACACACTCATGAAGAAAGAAACACAGGATAGC 1852
421 TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTTCCCTCTACCCCTATTCCTCAATCT 480
1853 TGAGAGGCTAAACTCATCAAAAACACTACTCTCTTTTCCCTCTACCCCTATTCCTCAATCT 1912
481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTCCTTTCTTTCTTACTCCCTCTCTCC 540
1913 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTCCTTTCTTTCTTACTCCCTCTCTCC 1972
541 TTTTACCCCTCCATGTCGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTCTGTA 600
1973 TTTTACCCCTCCATGTCGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTCTGTA 2032
601 CACAGTTATACATGCTATCAAAACCAGACTTGCCTTCCATAGTGGAGCTCTCTTTTCAG 660
2033 CACAGTTATACATGCTATCAAAACCAGACTTGCCTTCCATAGTGGAGCTCTCTTTTCAG 2092
661 AACATAGGAGTAAGTGAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 720
2093 AACATAGGAGTAAGTGAAGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTTCAGAGATT 2152
721 AAGTTATTTTATATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 780
2153 AAGTTATTTTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2211
781 TGTGTGTGATGCTGCTGTGTAGACACACAGCATACACATATATATATATATATATAT 840
2212 -GTGTGTGATGCTGCTGTGTAGACACACAGCATACACATATATATATATATATATAT 2270
841 AGCCATTTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGATGATTTTCAAGAGCA 900
2271 AGCCATTTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGATGATTTTCAAGAGCA 2330
901 AGATTGGCATATCATTGTAACATAAAAGCTGACATGACACAGATATGATCTCTTT 960
2331 AGATTGGCATATCATTGTAACATAAAAGCTGACATGACACAGATATGATCTCTTT 2390
961 CTAAAAATAATAATAATGCTACAGAAAGAGAGACCGTTCGTTTGGCAATCTACAG 1020
2391 CTAAAAATAATAATAATGCTACAGAAAGAGAGACCGTTCGTTTGGCAATCTACAG 2450
1021 CTAGTAGAGACTTTGAGGAAGAATTTCAACAGTGTGTCTTTCAGCAGTGTTCAGAGCCNAGC 1080
2451 CTAGTAGAGACTTTGAGGAAGAATTTCAACAGTGTGTCTTTCAGCAGTGTTCAGAGCCNAGC 2510
1081 AAGAAAGTTGAAGTTGCTTAGACAGAGCATAAAGTATCATGTCTCTTTTAACTAGCATTA 1140
2511 AAGAAAGTTGAAGTTGCTTAGACAGAGCATAAAGTATCATGTCTCTTTTAACTAGCATTA 2570
1141 CCCCAAGTGGAGAGGGTGCAGAGGCTCAAGGCATTAAGTCAATTCAGCCACT 1200
2571 CCCCAAGTGGAGAGGGTGCAGAGGCTCAAGGCATTAAGTCAATTCAGCCACT 2630
1201 AAGTTGTCTCTTTCTGTTTCTGTTTCCATCGGAACATTTTGAATATAGTTTAACTCTTC 1260

2631 AAGTTGTCTCTTTCTGTTTCTGTTTCCATGGAACATTTTGTATTATAGTTAACTCCTTC 2690
1261 TATCTTGAATCTT 1273
2691 TATCTTGAATCTT 2703
RESULT 12
US-10-741-600-2
; Sequence 2, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: Pbatseq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2777)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-2
Query Match 98.9%; Score 1258.6; DB 21; Length 2777;
Best Local Similarity 99.8%; Pred. No. Se-296; Mismatches 0; Indels 2; Gaps 1;
Matches 1270; Conservative 1;
QY 1 GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTGTAGATTGTAATATATACATCTAT 60
DB 1439 GGCCTCTCACTAACTAACTCACTTTCCCATCTTTTGTAGATTGTAATATATACATCTAT 1498
QY 61 GATCATTTCTTTTCTTTTACAGGGGAGAAATTTTACATATTTTACCTGAGCAAAATGATTA 120
DB 1499 GATCATTTCTTTTCTTTTACAGGGGAGAAATTTTACATATTTTACCTGAGCAAAATGATTA 1558
QY 121 GAAATGGAACCACTAGAGGAATATAATGTTAGGAATACAGTCAATTTCTAAGGGCC 180
DB 1559 GAAATGGAACCACTAGAGGAATATAATGTTAGGAATACAGTCAATTTCTAAGGGCC 1618
QY 181 CAGCCCTTGACAAAATTTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATACATGGTTC 240
DB 1619 CAGCCCTTGACAAAATTTGGAAGTTAAATTTCTCCACTCTGTCCATCAGATACATGGTTC 1678
QY 241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTTAGCAGCATTCATCTTCCGAT 300
DB 1679 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCTTAGCAGCATTCATCTTCCGAT 1738
QY 301 CTTCTTTCTCTTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360
DB 1739 CTTCTTTCTCTTCCAAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 1798
QY 361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAAACACAGAGTAGC 420
DB 1799 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAAACACAGAGTAGC 1858
QY 421 TGAGAGGCTAAAACTCATCAAAAAACATPACTCTCTTTTCCCTCTACCCCTATTCCTCAATCT 480
DB 1859 TGAGAGGCTAAAACTCATCAAAAAACATPACTCTCTTTTCCCTCTACCCCTATTCCTCAATCT 1918
QY 481 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTCCTTTCTTCTTACTCCCTCTCTCC 540
DB 1919 TTACCTTTTCCAAATCCCAATCCCAATCAGTTTTCCTTTCTTCTTACTCCCTCTCTCC 1978
QY 541 TTTTACCCCTCCATGTCGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTGTA 600
DB 1979 TTTTACCCCTCCATGTCGTTAAAGGAGAGATGGGAGCATCATCTGTTTATATCTGTA 2038

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